



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification <sup>6</sup> : C12N 15/81, 1/16, C07K 14/39, C12N 9/02, 15/53, 15/52, 15/60, C12P 23/00, C12N 1/21 // (C12N 1/16, C12R 1:645) (C12N 1/21, C12R 1:19)</p>	A1	<p>(11) International Publication Number: WO 97/23633</p> <p>(43) International Publication Date: 3 July 1997 (03.07.97)</p>
<p>(21) International Application Number: PCT/EP96/05887</p> <p>(22) International Filing Date: 23 December 1996 (23.12.96)</p> <p>(30) Priority Data: 95203620.0 22 December 1995 (22.12.95) EP (34) Countries for which the regional or international application was filed: NL et al. 96200943.7 11 April 1996 (11.04.96) EP (34) Countries for which the regional or international application was filed: NL et al.</p> <p>(71) Applicants (for all designated States except US): GIST-BROCADES B.V. [NL/NL]; Wateringseweg 1, P.O. Box 1, NL-2600 MA Delft (NL). OOIJEN, Albert, Johannes, Joseph [NL/NL]; Overburgkade 78, NL-2275 XX Voorburg (NL).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): VERDOES, Jan, Cornelis [NL/NL]; Van der Wouwstraat 50, NL-6706 JS Wageningen (NL). WERY, Jan [NL/NL]; Dijkstraat 7, NL-6703 CH Wageningen (NL).</p>	<p>(74) Agents: KLEIN, Bart et al.; Gist-Brocades N.V., Patents and Trademarks Dept., Wateringseweg 1, P.O. Box 1, NL-2600 MA Delft (NL).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</p>	
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Improved methods for transforming *Phaffia* strains, transformed *Phaffia*  
strains so obtained and recombinant DNA in said methods

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Technical field

The present invention relates to methods for transforming *Phaffia* yeast, transformed *Phaffia* strains, as well as recombinant DNA for use therein.

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Background of the invention

Methods for transforming the yeast *Phaffia rhodozyma* have been disclosed in European patent application 0 590 707 A1. These methods involve incubation of protoplasts with DNA or incubation of *Phaffia* cells with DNA followed by lithium acetate treatment. The recombinant DNA used to transform *Phaffia* strains with either of these methods comprised a *Phaffia* actin gene promoter to drive expression of the selectable marker genes coding for resistance against G418 or phleomycin. The methods involve long PEG and lithium acetate incubation times and transformation frequencies are low. When protoplasts are used, the transformation frequency is dependent on the quality of the protoplast suspension, making the procedure less reliable.

Recently a method for transforming *Phaffia* strains has been reported by Adrio J.L. and Veiga M. (July 1995, Biotechnology Techniques Vol. 9, No. 7, pp. 509-512). With this method the transformation frequencies are in the range of 3 to 13 transformants per  $\mu\text{g}$  DNA, which is low. A further disadvantage of the method disclosed by these authors consists in increased doubling time of the transformed cells. The authors hypothesised that this may be due to interference of the autonomously replicating vector with chromosome replication.

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Clearly, there is still a need for a reliable and efficient method of transforming *Phaffia* strains with foreign DNA. It is an objective of the present invention to provide methods and means to achieve this. It is a further objective of the invention to optimize expression of certain genes in *Phaffia rhodozyma* in order to make *Phaffia* a more suitable production host for certain valuable compounds.

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Summary of the invention

The invention provides a method for obtaining a transformed *Phaffia* strain, comprising the steps of contacting cells or protoplasts of a *Phaffia* strain with recombinant DNA under conditions conducive to uptake thereof, said recombinant DNA comprising a transcription promoter and a downstream sequence to be expressed which is heterologous to said transcription promoter, in operable linkage therewith, identifying *Phaffia rhodozyma* cells or protoplasts having obtained the said recombinant DNA in expressible form, wherein the transcription promoter comprises a region that is found upstream of the open reading frame of a highly expressed *Phaffia* gene. According to a preferred embodiment of the invention said highly expressed *Phaffia* gene is a glycolytic pathway gene, more preferably the glycolytic pathway gene is coding for Glyceraldehyde-3-Phosphate Dehydrogenase



(GAPDH). According to one aspect of the invention, said heterologous downstream sequence comprises an open reading frame coding for resistance against a selective agent, such as G418 or phleomycin.

Another preferred method according to the invention is one, wherein said recombinant DNA comprises further a transcription terminator downstream from the said DNA to be expressed, in operable linkage therewith, which transcription terminator comprises a region found downstream of the open reading frame of a *Phaffia* gene. It is still further preferred, that the recombinant DNA is in the form of linear DNA.

Another preferred embodiment comprises, in addition to the steps above, the step of providing an electropulse after contacting of *Phaffia* cells or protoplasts with DNA.

According to another embodiment the invention provides a transformed *Phaffia* strain capable of high-level expression of a heterologous DNA sequence, which strain is obtainable by a method according to the invention. Preferably, said *Phaffia* strain contains at least 10 copies of the said recombinant DNA integrated into its genome, such as a chromosome, particularly in the ribosomal DNA locus of said chromosome.

The invention also provides recombinant DNA comprising a transcription promoter and a heterologous downstream sequence to be expressed, in operable linkage therewith, wherein the transcription promoter comprises a region found upstream of the open reading frame of a highly expressed *Phaffia* gene, preferably a glycolytic pathway gene, more preferably a gene coding for Glyceraldehyde-3-Phosphate Dehydrogenase.

Also provided is recombinant DNA according to the invention, wherein the heterologous downstream sequence comprises an open reading frame coding for reduced sensitivity against a selective agent, preferably G418 or phleomycin. Said recombinant DNA preferably comprises further a transcription terminator downstream from the said heterologous DNA sequence to be expressed, in operable linkage therewith.

Further aspects of the invention concern a microorganism harbouring recombinant DNA according to the invention, preferably *Phaffia* strains, more preferably *Phaffia rhodozyma* strains, as well as cultures thereof.

According to still other preferred embodiments isolated DNA fragments are provided comprising a *Phaffia* GAPDH-gene, or a fragment thereof, as well as the use of such a fragment for making a recombinant DNA construct. According to one embodiment of this aspect said fragment is a regulatory region located upstream or downstream of the open reading frame coding for GAPDH, and it is used in conjunction with a heterologous sequence to be expressed under the control thereof.

The invention according to yet another aspect, provides a method for producing a protein or a pigment by culturing a *Phaffia* strain under conditions conducive to the production of said protein or pigment, wherein the *Phaffia* strain is a transformed *Phaffia* strain according to the invention.

According to another aspect of the invention, a method for obtaining a transformed *Phaffia* strain, comprising the steps of

contacting cells or protoplasts of a *Phaffia* strain with recombinant DNA under conditions conducive to uptake thereof,

said recombinant DNA comprising a transcription promoter and a downstream sequence to be expressed in operable linkage therewith,

identifying *Phaffia rhodozyma* cells or protoplasts having obtained the said recombinant DNA in expressible form,

5 wherein the downstream sequence to be expressed comprises an isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia rhodozyma*. Preferably, said enzyme has an activity selected from geranylgeranyl pyrophosphate synthase (*crtE*), phytoene synthase (*crtB*), phytoene desaturase (*crtI*) and lycopene cyclase (*crtY*), more preferably an enzyme having an amino acid sequence selected from the one represented by SEQIDNO: 13, SEQIDNO: 15,  
10 SEQIDNO: 17 and SEQIDNO: 19. According to a further embodiment, the transcription promoter is heterologous to said isolated DNA sequence, such as a glycolytic pathway gene in *Phaffia*. Especially preferred according to this embodiment is the Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH) gene promoter.

Also provided is a transformed *Phaffia* strain obtainable by a method according to the  
15 invention and capable of expressing, preferably over-expressing the DNA sequence encoding an enzyme involved in the carotenoid biosynthesis pathway gene.

The invention is also embodied in recombinant DNA comprising an isolated DNA sequence according to the invention, preferably in the form of a vector.

Also claimed is the use of such a vector to transform a host, such as a *Phaffia* strain.

20 A host obtainable by transformation, optionally of an ancestor, using a method according to any one of claims 1 to 5, wherein said host is preferably capable of over-expressing DNA according to the invention.

According to a further embodiment a method is provided for expressing an enzyme involved in the carotenoid biosynthesis pathway, by culturing a host according to the invention under conditions  
25 conducive to the production of said enzyme. Also provided is a method for producing a carotenoid by cultivating a host according to the invention under conditions conducive to the production of carotenoid.

The following figures further illustrate the invention.

#### Description of the Figures

30 Fig. 1. Mapping of the restriction sites around the *Phaffia rhodozyma* GAPDH gene. Ethidium bromide stained 0.8 % agarose gel (A) and Southern blot of chromosomal DNA (B) and cosmid pPRGDHcos1 (C) digested with several restriction enzymes and hybridized with the 300-bp PCR fragment of the *Phaffia rhodozyma* GAPDH gene. Lane 1, DNA x *KpnI*; 2, x*PstI*; 3, x*SmaI*; 4, x*SphI*; L, lambda DNA digested with *BstEII*; 5, x*SstI*; 6, x*XbaI* and 7,  
35 x*XhoI*.

The blot was hybridized in 6 x SSC, 5 x Denhardt's, 0.1 % SDS, 100 ng/ml herring sperm DNA at 65°C and washed with 0.1 x SSC/0.1% SDS at 65°C. Exposure time of the autoradiogram was 16 h for the cosmid and 48 h from the blot containing the chromosomal DNA.

Fig. 2. The organisation of two subclones; pPRGDH3 and derivative (A) and pPRGDH6 and derivatives (B) containing (a part of) the GAPDH gene of *Phaffia rhodozyma*. The PCR probe is indicated by a solid box. The direction and extent of the sequence determination is indicated by arrows.

solid boxes: GAPDH coding sequence

open box: 5' upstream and promoter region of GAPDH

open box: 3' non-coding *Phaffia rhodozyma* GAPDH sequence

solid line: GAPDH intron

hatched box: Poly-linker containing sites for different restriction enzymes

dotted line: deleted fragments

Fig. 3. Cloning diagram of *Phaffia* transformation vector; pPR2.

solid box: 5' upstream and promoter sequence of GAPDH

hatched box: G418

solid line: pUC19

open box: ribosomal DNA of *Phaffia rhodozyma*

Only restriction sites used for cloning are indicated.

Fig. 4. Construction of pPR2T from pPR2T.

Solid box (*Bam*HI - *Hind*III fragment): GAPDH transcription terminator from *Phaffia*.

All other boxes and lines are as in Fig. 3. Only relevant details have been depicted.

Fig. 5. Detailed physical map of pGB-Ph9. bps = basepairs; rDNA ribosomal DNA locus of *Phaffia*; act.pro 2 = actin transcription promoter; act.1 5' non-translated and aminoterminal region of the open reading frame; NON COD. = non-coding region downstream of G418-gene;

Fig. 6. Detailed physical map of pPR2. GPDHpro = GAPDH transcription promoter region from *Phaffia*. Other acronyms as in Fig. 5.

Fig. 7. Detailed physical map of pPR2T. Tgdh = GAPDH transcription terminator of *Phaffia*. All other acronyms as in Fig. 5 and 6.

Fig. 8. Overview of the carotenoid biosynthetic pathway of *Erwinia uredovora*.

Fig. 9. Representation of cDNA fragments and a restriction enzyme map of the plasmids pPRcrtE (A); pPRcrtB (B), pPRcrtI (C) and pPRcrtY (B).

#### Detailed description of the invention

The invention provides in generalised terms a method for obtaining a transformed *Phaffia* strain, comprising the steps of

contacting cells or protoplasts of a *Phaffia* strain with recombinant DNA under conditions conducive to uptake thereof,

said recombinant DNA comprising a transcription promoter and a downstream sequence to be expressed which is heterologous to said transcription promoter, in operable linkage therewith,

identifying *Phaffia rhodozyma* cells or protoplasts having obtained the said recombinant DNA in expressible form,

wherein the transcription promoter comprises a region that is found upstream of the open reading frame of a highly expressed *Phaffia* gene.

In order to illustrate the various ways of practicing the invention, some embodiments will be high-lighted and the meaning or scope of certain phrases will be elucidated.

5 The meaning of the expression recombinant DNA is well known in the art of genetic modification, meaning that a DNA molecule is provided, single or double stranded, either linear or circular, nicked or otherwise, characterised by the joining of at least two fragments of different origin. Such joining is usually, but not necessarily done *in vitro*. Thus, within the ambit of the claim are molecules which comprise DNA from different organisms or different genes of the same organism, or  
10 even different regions of the same gene, provided the regions are not adjacent in nature. The recombinant DNA according to the invention is characterised by a transcription promoter found upstream of an open reading frame of a highly expressed *Phaffia* gene, fused to a heterologous DNA sequence. With heterologous is meant 'not naturally adjacent'. Thus the heterologous DNA sequence may be from a different organisms, a different gene from the same organism, or even of the same gene as the  
15 promoter, provided that the downstream sequence has been modified, usually *in vitro*. Such modification may be an insertion, deletion or substitution, affecting the encoded protein and/or its entrance into the secretory pathway, and/or its post-translational processing, and/or its codon usage.

The strong transcription promoter according to the invention must be in operable linkage with the heterologous downstream sequence in order to allow the transcriptional and translational machinery  
20 to recognise the starting signals. The regions upstream of open reading frames of highly expressed *Phaffia* genes contain TATA-like structures which are positioned at 26 to about 40 nucleotides upstream of the cap-site; the latter roughly corresponds with the transcriptional start site. Thus in order to allow transcription of the heterologous downstream sequence to start at the right location similar distances are to be respected. It is common knowledge, however, that there is a certain tolerance in the location of the  
25 TATA-signal relative to the transcription start site. Typically, mRNAs of the eukaryotic type contain a 5'-untranslated leader sequence (5'-utl), which is the region spanning the transcription start site to the start of translation; this region may vary from 30 to more than 200 nucleotides. Neither the length nor the origin of the 5'-utl is very critical; preferably it will be between 30 and 200 nucleotides. It may be from the same gene as the promoter, or it may be from the gene coding for the heterologous protein. It  
30 is well known that eukaryotic genes contain signals for the termination of transcription and/or polyadenylation, downstream of the open reading frame. The location of the termination signal is variable, but will typically be between 10 and 200 nucleotides downstream from the translational stop site (the end of the open reading frame), more usually between 30 and 100 nucleotides downstream from the translational stop site. Although the choice of the transcription terminator is not critical, it is found,  
35 that the when the terminator is selected from a region downstream of a *Phaffia* gene, preferably of a highly expressed *Phaffia* gene, more preferably from the GAPDH-encoding gene, the level of expression, as well as the frequency of transformation is improved.

It was found that significant numbers of clones were obtained which could grow on very high G418 concentrations (up to, and over, 1 mg/ml). Transcription promoters according to the invention are

said to be from highly expressed genes, when they can serve to allow growth of transformed *Phaffia* cells, when linked to a G418 resistance gene as disclosed in the Examples, in the presence of at least 200 µg/ml, preferably more than 400, even more preferably more than 600, still more preferably more than 800 µg/ml of G418 in the growth medium. Examples of such promoters are, in addition to the promoter upstream from the GAPDH-gene in *Phaffia*, the promoters from *Phaffia* genes which are homologous to highly expressed genes from other yeasts, such as *Pichia*, *Saccharomyces*, *Kluyveromyces*, or fungi, such as *Trichoderma*, *Aspergillus*, and the like. Promoters which fulfill the requirements according to the invention, may be isolated from genomic DNA using molecular biological techniques which are, as such, all available to the person skilled in the art. The present invention provides a novel strategy for isolating strong promoters from *Phaffia* as follows. A cDNA-library is made from *Phaffia* mRNA, using known methods. Then for a number of clones with a cDNA insert, the DNA fragment (which represents the cDNA complement of the expressed mRNA) is sequenced. As a rule all fragments represent expressed genes from *Phaffia*. Moreover, genes that are abundantly expressed (such as the glycolytic promoters) are overrepresented in the mRNA population. Thus, the number of DNA-fragments to be sequenced in order to find a highly expressed gene, is limited to less than 100, probably even less than 50. The sequencing as such is routine, and should not take more than a couple of weeks. The nucleotide sequences obtained from this limited number of fragments, is subsequently compared to the known sequences stored in electronic databases such as EMBL or Geneseq. If a fragment shows homology of more than 50% over a given length (preferably more than 100 basepairs) the fragment is likely to represent the *Phaffia* equivalent of the gene found in the electronic database. In yeasts other than *Phaffia*, a number of highly expressed genes have been identified. These genes include the glycolytic pathway genes, phosphoglucose isomerase, phosphofructokinase, phosphotriose isomerase, phosphoglucose mutase, enolase, pyruvate kinase, alcohol dehydrogenase genes (EP 120 551, EP 0 164 556; Rosenberg S. *et al.*, 1990, *Meth. Enzymol.*: 185, 341-351; Tuite M.F. 1982, *EMBO J.* 1, 603-608; Price V. *et al.*, 1990, *Meth. Enzymol.* 185, 308-318) and the galactose regulon (Johnston, S.A. *et al.*, 1987, *Cell* 50, 143-146). Accordingly, those *Phaffia* cDNA fragments that are significantly homologous to the highly expressed yeast genes (more than 40%, preferably more than 50% identity in a best match comparison over a range of more than 50, preferably more than 100 nucleotides) should be used to screen a genomic library from *Phaffia*, to find the corresponding gene. Employing this method, 14 highly expressed mRNAs from *Phaffia rhodozyma* have been copied into DNA, sequenced, and their (putative) open reading frames compared to a nucleic acid and amino acid sequence databases. It turned out that 13 out of these fourteen cDNAs coded for ribosomal protein genes, of which one coded simultaneously to ubiquitin; one cDNA codes for a glucose-repressed gene. The isolation of the genes and the promoters usually found upstream of the coding regions of these genes is now underway, and it is anticipated that each of these transcription promoters may advantageously be used to express heterologous genes, such as carotenoid biosynthesis genes. Among the genes and transcription promoters especially preferred according to this invention are the promoter found upstream of the ubiquitin-ribosomal 40S protein corresponding to the cDNA represented in SEQIDNO:10, the glucose-repressed cDNA represented in SEQIDNO:26, the 40S ribosomal protein S27 encoding cDNA represented in

SEQIDNO:28, the 60S ribosomal protein P1 $\alpha$  encoding cDNA represented by SEQIDNO:30, the 60S ribosomal protein L37e encoding cDNA represented in SEQIDNO:32, the 60S ribosomal protein L27a encoding cDNA represented in SEQIDNO:34, the 60S ribosomal protein L25 encoding cDNA represented in SEQIDNO:36, the 60S ribosomal protein P2 encoding cDNA represented in SEQIDNO:38, the 40S ribosomal protein S17A/B encoding cDNA represented in SEQIDNO:40, the 40S ribosomal protein S31 encoding cDNA represented in SEQIDNO:42, the 40S ribosomal protein S10 encoding cDNA represented in SEQIDNO:44, the 60S ribosomal protein L37A encoding cDNA represented in SEQIDNO:46, the 60S ribosomal protein L34 encoding cDNA represented in SEQIDNO:48, or the 40S ribosomal protein S16 encoding cDNA represented in SEQIDNO:50.

10 Promoters from these or other highly expressed genes can be picked up by the method according to the invention using only routine skills of (a) making a cDNA library on mRNA isolated from a *Phaffia* strain grown under desired conditions, (b) determining (part of) the nucleotide sequence of the (partial) cDNAs obtained in step (a), (c) comparing the obtained sequence data in step (b) to known sequence data, such as that stored in electronic databases, (d) cloning putative promoter fragments  
15 of the gene located either directly upstream of the open reading frame or directly upstream of the transcription start site of the gene corresponding to the expressed cDNA, and (e) verifying whether promoter sequences have been obtained by expressing a suitable marker, such as the G418 resistance gene, or a suitable non-selectable "reporter" sequence downstream from a fragment obtained in (d), transforming the DNA into a *Phaffia rhodozyma* strain and determining the level of expression of the  
20 marker gene or reporter sequence of transformants. A transcriptional promoter is said to be of a highly expressed gene if it is capable of making *Phaffia rhodozyma* cells transformed with a DNA construct comprising the said promoter linked upstream of the G418 resistance marker resistant to G418 in concentrations exceeding 200  $\mu$ g per liter culture medium, preferably at least 400, more preferably more than 600  $\mu$ g/l. Especially preferred promoters are those conferring resistance against more than 800  
25  $\mu$ g/ml G418 in the growth medium.

Optionally, the transcriptional start site may be determined of the gene corresponding to the cDNA corresponding to a highly expressed gene, prior to cloning the putative promoter sequences; this may serve to locate the transcriptional initiation site more precisely, and moreover, helps to determine the length of the 5'-non-translated leader of the gene. To determine the location of the transcription start  
30 site, reverse primer extension, or classical S1-mapping may be performed, based on the knowledge of the cDNA sequence. Thus the exact location of the transcription promoter can be determined without undue burden, and the isolation of a fragment upstream of the transcription start site and containing the promoter, from a hybridising genomic clone (for example a phage or cosmid) is routine. Cloning the putative promoter fragment in front (upstream) of the coding region of, for example the G418-resistance  
35 gene, and transforming the gene cassette to *Phaffia* in order to evaluate the level of G418 resistance, and hence the level of expression of the G418-resistance gene as a consequence of the presence of the promoter is routine.

In a manner essentially as described for the isolation of other strong promoters, above, a transcription terminator may be isolated, with the proviso, that the terminator is located downstream

from the open reading frame. The transcription stop site can be determined using procedures which are essentially the same as for the determination of the transcription start site. All these procedures are well known to those of skill in the art. A useful handbook is Nucleic Acid Hybridisation, Edited by B.D. Hames & S.J. Higgins, IRL Press Ltd., 1985; or Sambrook, *sub*. However, it is not critical that the transcription terminator is isolated from a highly expressed *Phaffia* gene, as long as it is from an expressed gene.

Using recombinant DNA according to the invention wherein the open reading frame codes for reduced sensitivity against G418, a transformation frequency was obtained up to 160 transformants per  $\mu\text{g}$  of linear DNA, at a G418 concentration in the medium of 40  $\mu\text{g/ml}$ .

About 10 to 20 times as much transformed colonies were obtained with the vector according to the invention (pPR2) than with the prior art vector pGB-Ph9, disclosed in EP 0 590 707 A1 (see Table 2; in the experiment of Example 7, the improvement is even more striking).

The method according to the invention calls for conditions conducive to uptake of the recombinant DNA. Such conditions have been disclosed in EP 509 707. They include but are not limited to the preparation of protoplasts using standard procedures known to those of skill in the art, and subsequent incubation with the recombinant DNA. Alternatively, *Phaffia* cells may be incubated overnight in the presence of LiAc and recombinant DNA. Still further alternative methods involve the use of particle acceleration. According to a preferred embodiment, the conditions conducive to uptake involve electroporation of recombinant DNA into *Phaffia* cells, such as described by Faber et al., (1994, Current Genetics 25, 305-310). Especially preferred conditions comprise electroporation, wherein the recombinant DNA comprises *Phaffia* ribosomal DNA, said recombinant DNA being in the linear form, most preferably by cleaving said recombinant DNA in the said ribosomal region. Still further preferred conditions, comprise the use of recombinant DNA in amounts of between 1 and 10  $\mu\text{g}$  per  $10^8$  cells, more preferably about 5  $\mu\text{g}$  recombinant DNA is used per  $2 \times 10^8$  cells, which are cultivated for 16 h at 21°C.

Once cells have been transformed according to the method, identification of transformed cells may take place using any suitable technique. Thus, identification may be done by hybridisation techniques, DNA amplification techniques such a polymerase chain reaction using primers based on the recombinant DNA used, and the like. A preferred method of identifying transformed cells is one which employs selection for the recombinant DNA that comprises a gene coding for reduced sensitivity against a selective agent. A useful selective agent is G418, hygromycin, phleomycin and *amdS*. Genes that code for reduced sensitivity against these selective agents are well known in the art. The open reading frames of these genes may be used as the heterologous downstream sequence according to the invention, allowing selective enrichment of transformed cells, prior to identification of transformed cells. Once transformed cells have been identified they may used for further manipulation, or used directly in the production of valuable compounds, preferably in large scale fermentors.

It will be clear, that a very efficient method for transforming *Phaffia* strains has been disclosed. Moreover, not only the frequency of transformation is high, the expression levels of the transforming DNA is very high as well, as is illustrated by the exceptionally high resistance against

G418 of the transformed *Phaffia* cells when the open reading frame of the G418-resistance gene was fused to a promoter according to the invention when compared to the G418 resistance gene under control of the actin promoter in pGB-Ph9. It is concluded, therefore, that the GAPDH-promoter is a high-level transcriptional promoter that can be suitably used in conjunction with any heterologous DNA sequence, in order to reach high expression levels thereof in *Phaffia* strains.

It will be clear that the availability of new expression tools, in the form of the recombinant DNA according to the invention, creates a wealth of possibilities for producing new and valuable biomolecules in *Phaffia*.

Preferably, the downstream sequence comprises an open reading frame coding for proteins of interest. For example genes already present in *Phaffia*, such as those involved in the carotenoid pathway, may be manipulated by cloning them under control of the high-level promoters according to the invention. Increased expression may change the accumulation of intermediates and/or end-products or change the pathway of  $\beta$ -carotene, cantaxanthin, astaxanthin and the like. The overexpression of the *crtB* gene from *Erwinia uredovora* will likely increase astaxanthin levels, as the product of this gene is involved in the rate limiting step. The expression of a protein of interest may also give rise to xanthophylls not known to be naturally produced in *Phaffia*, such as zeaxanthin. An open reading frame that may be suitably employed in such a method includes but is not limited to the one encoding the protein producing zeaxanthin (*crtZ* gene) obtained from *Erwinia uredovora* (Misawa et al.1990. J.Bacteriol. 172 : 6704-6712). Other carotenoid synthesis genes can be obtained for example from *Flavobacterium* (a gram-positive bacterium), *Synechococcus* (a cyanobacterium) or *Chlamydomonas* or *Dunaliella* (algae). Obviously, carotenoid synthesis genes of a *Phaffia* strain, once the genes have been isolated and cloned, are suitably cloned into a recombinant DNA according to the invention and used to modify the carotenoid content of *Phaffia* strains. Examples of cloned carotenoid genes that can suitably be overexpressed in *Phaffia*, are those mentioned in Fig. 8. Particularly useful is *crtE* from *Phycomyces blakesleanus*, encoding Geranylgeranyl Diphosphate Synthase, and *crtB*, encoding phytoene synthase, as this step appears to be the rate-limiting step in carotenoid synthesis in *Thermus thermophilus* (Hoshino T. et al., 1994, Journal of Fermentation and Bioengineering 77, No. 4, 423-424). Especially preferred sources to isolate carotenoid biosynthetic genes or cDNAs from are the fungi *Neurospora crassa*, *Blakeslea trispora*. Other yeasts shown to possess cross-hybridising species of carotenoid biosynthetic genes are *Cystofylobasidium*, e.g. *bisporidii* and *capitatum*.

Carotenoid biosynthesis genes have also been identified in plants; these plant cDNAs or genes from plants may be used as well. Optionally, the codon usage of the *Phaffia* genes or cDNAs may be adapted to the preferred use in the host organism.

Of special interest according to the present invention, are the DNA sequences coding for four different enzymes in the carotenoid biosynthesis pathway of *Phaffia rhodozyma*, represented in the sequence listing. It will be clear to those having ordinary skill in the art, that once these DNA sequences have been made available it will be possible to bring about slight modifications to the DNA sequence without modifying the amino acid sequence. Such modifications are possible due to the degeneracy of the genetic code. Such modifications are encompassed in the present invention. However, also



modifications in the coding sequences are envisaged that create modifications in the amino acid sequence of the enzyme. It is well known to those of skill in the art that minor modifications are perfectly permissible in terms of enzymatic activity. Most changes, such as deletions, additions or amino acid substitutions do not affect enzymatic activity, at least not dramatically. Such variants as comprise one or more amino acid deletions, additions or substitutions can readily be tested using the complementation test disclosed in the specification. The skilled person is also familiar with the term "conservative amino acid substitutions", meaning substitutions of amino acids by similar amino acids residing in the same group. The skilled person is also familiar with the term "allelic variant", meaning naturally occurring variants of one particular enzyme. These conservative substitutions and allelic enzyme variants do not depart from the invention.

As stated, at the DNA level considerable variation is acceptable. Although the invention discloses four DNA sequences, as represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16, SEQIDNO: 18, SEQIDNO: 20, or SEQIDNO: 22, in detail also isocoding variants of the DNA sequence represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16, SEQIDNO: 18, SEQIDNO: 20, or SEQIDNO: 22, are encompassed by the present invention. Those of skill in the art would have no difficulty in adapting the nucleic acid sequence in order to optimize codon usage in a host other than *P. rhodozyma*. Those of skill in the art would know how to isolate allelic variants of a DNA sequence as represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16, SEQIDNO: 18, SEQIDNO: 20, or SEQIDNO: 22 from related *Phaffia* strains. Such allelic variants clearly do not deviate from the present invention.

Furthermore, using the DNA sequences disclosed in the sequence listing, notably SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16 or SEQIDNO: 18, as a probe, it will be possible to isolate corresponding genes from other strains, or other microbial species, or even more remote eukaryotic species if desired, provided that there is enough sequence homology, to detect the same using hybridisation or amplification techniques known in the art.

Typically, procedures to obtain similar DNA fragments involve the screening of bacteria or bacteriophage plaques transformed with recombinant plasmids containing DNA fragments from an organism known or expected to produce enzymes according to the invention. After *in situ* replication of the DNA, the DNA is released from the cells or plaques, and immobilised onto filters (generally nitro-cellulose). The filters may then be screened for complementary DNA fragments using a labeled nucleic acid probe based on any of the sequences represented in the sequence listing. Dependent on whether or not the organism to be screened for is distantly or closely related, the hybridisation and washing conditions should be adapted in order to pick up true positives and reduce the amount of false positives. A typical procedure for the hybridisation of filter-immobilised DNA is described in Chapter 5, Table 3, pp. 120 and 121 in: *Nucleic acid hybridisation- a practical approach*, B.D. Hames & S.J. Higgins Eds., 1985, IRL Press, Oxford). Although the optimal conditions are usually determined empirically, a few useful rules of thumb can be given for closely and less closely related sequences.

In order to identify DNA fragments very closely related to the probe, the hybridisation is performed as described in Table 3 of Hames & Higgins, *supra*, (the essentials of which are reproduced

below) with a final washing step at high stringency in 0.1 \* SET buffer (20 times SET = 3M NaCl, 20 mM EDTA, 0.4 M Tris-HCl, pH 7.8), 0.1% SDS at 68° Celsius).

To identify sequences with limited homology to the probe the procedure to be followed is as in Table 3 of Hames & Higgins, *supra*, but with reduced temperature of hybridisation and washing. A final wash at 2 \* SET buffer, 50°C for example should allow the identification of sequences having about 75% homology. As is well known to the person having ordinary skill in the art, the exact relationship between homology and hybridisation conditions depend on the length of the probe, the base composition (% of G + C) and the distribution of the mismatches; a random distribution has a stronger decreasing effect on  $T_m$  than a non-random or clustered pattern of mismatches.

The essentials of the procedure described in Table 3, Chapter 5 of Hames & Higgins are as follows:

(1) prehybridisation of the filters in the absence of probe, (2) hybridisation at a temperature between 50 and 68°C in between 0.1 and 4 \* SET buffer (depending on the stringency), 10 \* Denhardt's solution (100 \* Denhardt's solution contains 2% bovine serum albumin, 2% Ficoll, 2% polyvinylpyrrolidone), 0.1% SDS, 0.1% sodiumpyrophosphate, 50 µg/ml salmon sperm DNA (from a stock obtainable by dissolving 1 mg/ml of salmon sperm DNA, sonicated to a length of 200 to 500 bp, allowed to stand in a water bath for 20 min., and diluted with water to a final concentration of 1 mg/ml); hybridisation time is not too critical and may be anywhere between 1 and 24 hours, preferably about 16 hours (o/n); the probe is typically labeled by nick-translation using  $^{32}\text{P}$  as radioactive label to a specific activity of between  $5 * 10^7$  and  $5 * 10^8$  c.p.m./µg; (3) (repeated) washing of the filter with 3 \* SET, 0.1% SDS, 0.1% sodiumpyrophosphate at 68°C at a temperature between 50°C and 68°C (dependent on the stringency desired), repeated washing while lowering the SET concentration to 0.1%, wash once for 20 min. in 4 \* SET at room temperature, drying filters on 3MM paper, exposure of filters to X-ray film in a cassette at -70°C for between 1 hour and 96 hours, and developing the film.

Generally, volumina of prehybridisation and hybridisation mixes should be kept at a minimum. All "wet" steps may be carried out in little sealed bags in a pre-heated water bath.

The above procedure serves to define the DNA fragments said to hybridise according to the invention. Obviously, numerous modifications may be made to the procedure to identify and isolate DNA fragments according to the invention. It is to be understood, that the DNA fragments so obtained fall under the terms of the claims whenever they can be detected following the above procedure, irrespective of whether they have actually been identified and/or isolated using this procedure.

Numerous protocols, which can suitably be used to identify and isolate DNA fragments according to the invention, have been described in the literature and in handbooks, including the quoted Hames & Higgins, *supra*.

With the advent of new DNA amplification techniques, such as direct or inverted PCR, it is also possible to clone DNA fragments *in vitro* once sequences of the coding region are known.

Also encompassed by the claims is a DNA sequence capable, when bound to nitrocellulose filter and after incubation under hybridising conditions and subsequent washing, of specifically hybridising to a radio-labelled DNA fragment having the sequence represented in SEQIDNO: 12.

SEQIDNO: 14, SEQIDNO: 16 or SEQIDNO: 18, as detectable by autoradiography of the filter after incubation and washing, wherein said incubation under hybridising conditions and subsequent washing is performed by incubating the filter-bound DNA at a temperature of at least 50°C, preferably at least 55°C, more preferably at least 60°C in the presence of a solution of the said radio-labeled DNA in 0.3 M NaCl, 40 mM Tris-HCl, 2 mM EDTA, 0.1% SDS, pH 7.8 for at least one hour, whereafter the filter is washed at least twice for about 20 minutes in 0.3 M NaCl, 40 mM Tris-HCl, 2 mM EDTA, 0.1% SDS, pH 7.8, at a temperature of 50°C, preferably at least 55°C, more preferably at least 60°C, prior to autoradiography.

The heterologous DNA sequence according to the invention may comprise any open reading frame coding for valuable proteins or their precursors, like pharmaceutical proteins such as human serum albumin, IL-3, insulin, factor VIII, tPA, EPO,  $\alpha$ -interferon, and the like, detergent enzymes, such as proteases and lipases and the like, cell wall degrading enzymes, such as xylanases, pectinases, cellulases, glucanases, polygalacturonases, and the like, and other enzymes which may be useful as additives for food or feed (e.g. chymosin, phytases, phospholipases, and the like). Such genes may be expressed for the purpose of recovering the protein in question prior to subsequent use, but sometimes this may not be necessary as the protein may be added to a product or process in an unpurified form, for example as a culture filtrate or encapsulated inside the *Phaffia* cells.

The yeast cells containing the carotenoids can be used as such or in dried form as additives to animal feed. Furthermore, the yeasts can be mixed with other compounds such as proteins, carbohydrates or oils.

Valuable substances, such as proteins or pigments produced by virtue of the recombinant DNA of the invention may be extracted. Carotenoids can also be isolated for example as described by Johnson et al. (Appl. Environm. Microbiol. 35: 1155-1159 (1978)).

Purified carotenoids can be used as colorants in food and/or feed. It is also possible to apply the carotenoids in cosmetics or in pharmaceutical compositions.

The heterologous downstream sequence may also comprise an open reading frame coding for reduced sensitivity against a selective agent. The open reading frame coding for an enzyme giving G418 resistance was used satisfactorily in the method according to the invention, but the invention is not limited to this selection marker. Other useful selection markers, such as the phleomycin resistance gene may be used, as disclosed in EP 590 707. Each of these genes is advantageously expressed under the control of a strong promoter according to the invention, such as the GAPDH-promoter.

The invention is now being illustrated in greater detail by the following non-limitative examples.

#### Experimental

Strains: *E. coli* DH5 $\alpha$ : *supE44lacU169* (80*lacZ*M15) *hsdR17 recA1 endA1 gyrA96 thi-1 relA1*  
*E. coli* LE392: *supE44 supF58 hsdR514 galK2 galT22 metB1 trpR55 lacY1*  
*P. rhodozyma* CBS6938

#### Plasmids:

pUC19 (Gibco BRL)

pTZ19R

PUC-G418

pGB-Ph9 (Gist-brocades)

pMT6 (1987, Breter H.-J., Gene 53, 181-190))

5 Media: LB: 10 g/l bacto tryptone, 5 g/l yeast extract, 10 g/l NaCl. Plates; +20 g/l bacto agar. When appropriate 50 µg/ml ampicillin.

YePD: 10 g/l yeast extract, 20 g/l bacto peptone, 20 g/l glucose. Plates; +20 g/l bacto agar. When appropriate 50 µg/ml Geneticin (G418).

Methods: All molecular cloning techniques were essentially carried out as described by Sambrook *et al.* in Molecular Cloning: a Laboratory Manual, 2nd Edition (1989; Cold Spring Harbor Laboratory Press).

Enzyme incubations were performed following instructions described by the manufacturer. These incubations include restriction enzyme digestion, dephosphorylation and ligation (Gibco BRL).

Isolation of chromosomal DNA from *Phaffia rhodozyma* as described in example 3 of patent Gist-brocades; EP 0 590 707 A1. Chromosomal DNA from *K. lactis* and *S.cerevisiae* was isolated as described by Cryer *et al.*(Methods in Cell Biology 12: 39, Prescott D.M. (ed.) Academic Press, New York).

Isolation of large (> 0.5-kb) DNA fragments from agarose was performed using the GeneClean II Kit whereas small (< 0.5-kb) and DNA fragments or fragments from PCR mixtures were isolated using Wizard™ DNA Clean-Up System (Promega).

20 Transformation of *E. coli* was performed according to the CaCl<sub>2</sub> method described by Sambrook *et al.* Packaging of cosmid ligations and transfection to *E. coli* LE392 was carried out using the Packagene Lambda DNA Packaging System (Promega), following the Promega protocols.

Isolation of plasmid DNA from *E. coli* was performed using the QIAGEN (Westburg B.V. NL).

25 Transformation of *Phaffia* CBS6938 was done according to the method for *H. polymorpha* described by Faber *et al.*, *supra*;

- Inoculate 30 ml of YePD with 1 CBS6938 colony
- Grow 1-2 days at 21°C, 300 rpm (pre-culture)
- Inoculate 200 ml of YePD with pre-culture to OD<sub>600</sub> = between 0 and 1 (if above 1 dilute with water)
- 30 - Grown o/n at 21°C, 300 rpm until OD<sub>600</sub> = 1.2 (dilute before measuring)
- Centrifuge at 5 min. 8000 rpm, room temperature. Remove supernatant thoroughly
- Resuspend pellet in 25 ml 50 mM KPi pH 7.0, 25 mM DTT (freshly made)

Transfer suspension to a fresh sterile 30 ml centrifuge tube and incubate for 15 min. at room temperature

- Centrifuge 5 min. at 8000 rpm 4°C, remove supernatant thoroughly
- 35 - Resuspend pellet in 25 ml of ice cold STM (270 mM sucrose, 10 mM Tris pH 7.5, 1 mM MgCl<sub>2</sub>)
- Centrifuge 5 min. at 8000 rpm, 4°C
- Repeat washing step
- Resuspend cells in 0.5 ml of ice cold STM (3\*10<sup>9</sup> cells/ml). Keep on ice!

- Transfer 60 µl of cell suspension to pre-cooled Eppendorf tubes containing 5 µg transforming DNA (use precooled tips!), Keep on ice
- Transfer Cell/DNA mix to precooled electroporation cuvettes (top to bottom)
- Pulse: 1.5 kV, 400 Ω, 25 µF
- 5 - Immediately add 0.5 ml of ice cold YePD. Transfer back to ep using a sterile Pasteur pipette
- Incubate 2.5 hrs at 21°C
- Plate 100 µl onto YePD-plates containing 40 µg/ml G418
- Incubate at 21°C until colonies appear.

Pulsed Field Electrophoresis was performed using a GENE Navigator + accessories (Pharmacia). Conditions: 0.15 \* TBE, 450 V, pulse time 0.5 s, 1.2% agarose, run time 2 h.

Polymerase Chain Reaction (PCR) experiments were performed in mixtures having the following composition:

- 5 ng of plasmid DNA or 1 µg chromosomal DNA
- 0.5 µg of oligo nucleotides (5 µg degenerated oligo's in combination with chromosomal DNA)
- 15 - 10 nm of each dNTP
- 2.5 µm KCl
- 0.5 µm Tris pH 8.0
- 0.1 µm MgCl<sub>2</sub>
- 20 - 0.5 µg gelatin
- 1.3 U *Taq* polymerase (5 U in combination with chromosomal DNA)

H<sub>2</sub>O was added to a total volume of 50 µl

Reactions were carried out in an automated thermal cycler (Perkin-Elmer).

Conditions: 5 min. 95°C, followed by 25 repeated cycles; 2' 94°C, 2' 45°C, 3' 72°C

25 Ending; 10 min. 72°C.

Fusion PCR reactions were performed as described above, except that 2 DNA fragments with compatible ends were added as a template in equimolar amounts.

Oligo nucleotide sequences were as follows:

30 3005: CGGGATCCAA(A/G)CTNACNGGNATGGC (SEQIDNO: 1);

3006: CGGGATCC(A/G)TAICC(C/A/G)(C/T)A(T/C)TC(A/G)TT(A/G)TC(A/G)TACCA (SEQIDNO: 2);

4206: GCGTGACTTCTGGCCAGCCACGATAGC (SEQIDNO: 3);

35 5126: TTCAATCCACATGATGGTAAGAGTGTTAGAGA (SEQIDNO: 4);

5127: CTTACCATCATGTGGATTGAACAAGATGGAT (SEQIDNO: 5);

5177: CCCAAGCTTCTCGAGGTACCTGGTGGGTGCATGTATGTAC (SEQIDNO: 6);

5137: CCAAGGCCTAAAACGGATCCCTCCAAACCC (SEQIDNO: 7);

5 5138: GCCAAGCTTCTCGAGCTTGATCAGATAAAGATAGAGAT (SEQIDNO: 8);

### Example 1

#### G-418 resistance of *Phaffia* transformant G418-1

To determine the expression of the G418 resistance gene in pGB-Ph9, transformant G418-1  
 10 (EP 0 590 707 A1) was exposed to increasing concentrations of G418.

Two dilutions of a G418-1 culture were plated onto YepD agar containing 0-1000 µg/ml G418  
 (Table I).

[G418] µg/ml	<i>Phaffia</i> G418-1 Dil.=10 <sup>-4</sup> (OD <sub>600</sub> =7)	<i>Phaffia</i> G418-1 Dil.=10 <sup>-5</sup> (OD <sub>600</sub> =7)	<i>Phaffia</i> (CBS6938) Dil.=0(OD <sub>600</sub> =5)
0	>300	74	>300
200	>300	70	0
300	>300	61	0
400	212	13	0
500	10	2	0
600	0	0	0
700	0	0	0
800	0	0	0
900	0	0	0
1000	0	0	0

25 **Table I.** Survival of *Phaffia* transformant G418-1 on YepD agar medium containing increasing concentrations of G418.

At a concentration of 600 µg/ml G418 less than 1% of the plated cells survived. It can be  
 30 concluded, that despite multicopy integration of pGB-Ph9, G418-1 shows a rather weak resistance to  
 G418 (Scorer *et al.*, 1994, Bio/Technology 12, p. 181 *et seq.*, Jimenez and Davies, 1980, Nature 187 p.  
 869 *et seq.*), most probably due to a weak action of the *Phaffia* actin promoter in the plasmid. The  
 results that the *Phaffia* actin promoter works poorly, prompted us to isolate promoter sequences of  
*Phaffia* with strong promoter activity.

### Example 2

#### Synthesis of specific probes of glycolytic genes from *Phaffia rhodozyma* by PCR

The polymerase chain reaction (PCR) technique was used in an attempt to synthesize a homologous probe of the genes encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK) and the triose phosphate isomerase (TPI) of *Phaffia rhodozyma*.

A set of degenerated oligonucleotides was designed based on the conserved regions in the GAPDH-gene (Michels *et al.*, 1986. EMBO J. 5: 1049-1056), PGK-gene (Osinga *et al.*, 1985. EMBO J. 4: 3811-3817) and the TPI-gene (Swinkels *et al.*, 1986. EMBO J. 5: 1291-1298).

All possible oligo combinations were used to synthesize a PCR-fragment with chromosomal DNA of *Phaffia rhodozyma* (strain CBS6938) as template. Chromosomal DNA of *Saccharomyces cerevisiae* and *Kluyveromyces lactis* as template was used to monitor the specificity of the amplification. The PCR was performed as described above, the PCR conditions were 1' 95 °C, 2' annealing temperature (T<sub>a</sub>), in 5' from annealing temperature to 72 °C, 2' 72 °C, for 5 cycli followed by 1' 95 °C, 2' 55 °C and 2' 72 °C for 25 cycli and another elongation step for 10' 72 °C. Three different T<sub>a</sub> were used 40 °C, 45 °C and 50 °C.

Under these conditions, only one primer combination produced a fragment of the expected size on chromosomal DNA of *Phaffia* as template. Using the oligo combination no: 3005 and 3006 and a T<sub>a</sub> of 45 °C a 0.3-kb fragment was found. Specifically, the GAPDH oligonucleotides correspond with amino acids 241-246 and 331-338 of the published *S. cerevisiae* sequence. (It was concluded that to isolate the promoters corresponding to the PGK- and TPI-genes from *Phaffia*, either further optimization of the PCR-conditions is required, or homologous primers should be used. Another alternative method for isolating high level promoters is disclosed in the detailed description, *supra*).

The amplified fragment was purified from the PCR reaction and was digested with *Bam*HI and ligated into the dephosphorylated *Bam*HI site of pTZ19R. The ligation mixture was transformed to competent *E. coli* DH5α cells prepared by the CaCl<sub>2</sub>-method and the cell were plated on LB-plates with 50 µg/ml Amp and 0.1 mM IPTG/50 µg/ml X-gal. Plasmid DNA was isolated from the white colonies. The pTZ19R clone with the right insert, called pPRGDH1, was subsequently used for sequence analysis of the insert.

The cloned sequence encoded for the carboxy terminal fragment of GAPDH of *Phaffia* as shown by comparison with the GAPDH-gene sequence of *S. cerevisiae* (Holland and Holland, 1979. J. of Biol. Chem. 254: 9839-9845).

### Example 3

#### Isolation of the GAPDH-gene of *Phaffia*

To obtain the complete GAPDH-gene including expression signals the 0.3-kb *Bam*HI fragment of pPRGDH1 was used to screen a cosmid library of *Phaffia*.

#### Preparation of the vector for cosmid cloning.

Vector preparation was simplified, because of the presence of a double cos-site in pMT6. PMT6 was digested to completion with blunt end cutter *PvuII* to release the cos-sites. Digestion efficiency was checked by transformation to *E. coli* DH5 $\alpha$  and found to be >99%.

The *PvuII* digested pMT6 was purified by phenol:chloroform extraction and ethanol  
5 precipitation and finally solved in 30  $\mu$ l TE at a concentration of 2  $\mu$ g/ $\mu$ l.

The vector was subsequently digested with cloning enzyme *Bam*HI and the vector arms were purified as described above ("Experimental").

#### Preparation of target DNA

10 Isolation of genomic DNA of *Phaffia* strain CBS6938 was performed as described in the part named "Experimental". The cosmid pMT6 containing inserts of 25-38-kb are most efficiently packaged. Therefore genomic DNA was subjected to partial digestion with the restriction enzyme *Sau*3A. Target DNA was incubated with different amounts of enzyme. Immediately after digestion the reactions were stopped by the extraction of DNA from the restriction mixture with phenol-chloroform. The DNA was  
15 precipitated by using the ethanol method and the pelleted DNA after centrifugation was dissolved in a small volume of TE. Contour clamped homogeneous electric field (CHEF) electrophoresis was used to estimate the concentration and size of the fragments (Dawkins, 1989, J. of Chromatography 492, pp. 615-639).

#### Construction of genomic cosmid library.

Ligation of approximately 0.5  $\mu$ g of vector arm DNA and 0.5  $\mu$ g of target DNA was performed in a total volume of 10  $\mu$ l in the presence of 5 mM ATP (to prevent blunt end ligation).

Packaging in phage heads and transfection to *E. coli* LE 392 as described in Experimental.

The primary library consisted of 7582 transfectants with an average insert of 28-kb as determined by  
25 restriction analysis. The library represents 3.5 times the genome with a probability of the presence of all genes in the library of 0.97 as calculated according to Sambrook (*supra*). For library amplification the transfectants were pooled by resuspending in 8 ml LB-broth. Additional 4.8 ml glycerol was added. The transfectants mixture was divided into 16 samples of 800  $\mu$ l each and stored at -80 °C. This amplified library consisted of  $2.9 \cdot 10^9$  transfectants.

30

#### Screening of the cosmid library.

A 100  $\mu$ l sample was taken from this library and further diluted ( $10^6$ ) in LB-broth and 200  $\mu$ l was plated onto 10 LB-plates containing ampicillin. The plates were incubated overnight at 37 °C. Each plate contained 300-400 colonies and filters were prepared. These filters were screened with the  
35 GAPDH-probe using hybridization and washing conditions as described above ("Experimental"). After 16 hours exposure, 3 strong hybridization signals were found on the autoradiogram.

Cosmid DNA isolated from these positive colonies was called pPRGDHcos1, pPRGDHcos2 and pPRGDHcos3.



Chromosomal DNA isolated from *Phaffia rhodozyma* strain CBS 6938 and cosmid pPRGDHcos1 was digested with several restriction enzymes. The DNA fragments were separated, blotted and hybridized as described before. The autoradiograph was exposed for different time periods at -80°C. The film showed DNA fragments of different length digested by different restriction enzymes which hybridize with the GAPDH-probe (Fig. 1).

Furthermore, from Southern analysis of the genomic DNA of *Phaffia* using the GAPDH fragment as probe, it was concluded that the GAPDH-encoding gene is present as a single copy gene in *Phaffia rhodozyma*, whereas in *Saccharomyces cerevisiae* GAPDH is encoded by three closely related but unlinked genes (Boucherie *et al.*, 1995. FEMS Microb. Letters 135:127-134).

Hybridizing fragments of pPRGDHcos1 for which a fragment of the same length in the chromosomal DNA digested with the same enzyme was found, were isolated from an agarose gel. The fragments were ligated into the corresponding sites in pUC19. The ligation mixtures were transformed to competent *E. coli* cells. The plasmids with a 3.3-kb *SalI* insert and a 5.5-kb *EcoRI* insert were called pPRGDH3 and pPRGDH6, respectively. The restriction map of pPRGDH3 and pPRGDH6 is shown in Figure 2. Analysis of the sequence data of the insert in pPRGDH1 showed us that there was a *HindIII* site at the C-terminal part of the GAPDH-gene. From this data it was suggested that the insert in pPRGDH6 should contain the complete coding sequence of GAPDH including promoter and terminator sequences.

#### Example 4

##### Characterization of the GAPDH-gene

In order to carry out sequence analysis without the need to synthesize a number of specific sequence primers a number of deletion constructs of plasmids pPRGDH3 and pPRGDH6 were made using convenient restriction sites in or near the putative coding region of GAPDH gene.

The plasmids were digested and after incubation a sample of the restriction mixture was analyzed by gel electrophoresis to monitor complete digestion. After extraction with phenol-chloroform the DNA was precipitated by ethanol. After incubation at -20 °C for 30' the DNA is pelleted by centrifugation, dried and dissolved in a large volume (0.1 ng/μl) of TE. After ligation the mixtures were transformed to *E. coli*. Plasmid DNA isolated from these transformants was analyzed by restriction analysis to reveal the right constructs. In this way the deletion constructs pPRGDH3δHIII, pPRGDH6δ*Bam*HI, pPRGDH6δ*Sst*I and pPRGDH6δ*Sal*I (Fig. 1).

In addition to this, the 0.6-kb and 0.8-kb *Sst*I fragments derived from pPRGDH6 were subcloned in the corresponding site of pUC19.

Sequence analysis was carried out using pUC/M13 forward and reverse primers (Promega). The sequencing strategy is shown in fig. 2 (see arrows).

On the basis of homology with the GAPDH-gene sequence of *S. cerevisiae* (Holland and Holland, 1979. J. of Biol. Chem. 254: 9839-9845) and *K. lactis* (Shuster, 1990. Nucl. Acids Res. 18, 4271) and the known splice site consensus J.L. Woolford, 1989. Yeast 5: 439-457), the introns and the possible ATG start were postulated.

The GAPDH gene has 6 introns (Fig. 1) and encodes a polypeptide of 339 amino acids. This was completely unexpected considering the genomic organisation of the GAPDH genes of *K. lactis* and *S. cerevisiae* which have no introns and both consist of 332 amino acids. The homology on the amino acid level between the GAPDH gene of *Phaffia* and *K. lactis* and *S. cerevisiae* is 63% and 61%, respectively.

Most of the introns in the GAPDH gene are situated at the 5' part of the gene. Except intron III all introns contain a conserved branch-site sequence 5'-CTPuAPy-3' found for *S. cerevisiae* and *S. pombe*.

By computer analysis of the upstream sequence using PC-gene 2 putative eukaryotic promoter elements, TATA-box (position 249-263 in SEQIDNO: 11) and a number of putative Cap signal (between position 287 and 302 in SEQIDNO: 11) were identified.

#### Example 5

##### Cloning of the GAPDH promoter fused to G418 in pUCG418.

In order to construct a transcription fusion between the GAPDH promoter and the gene encoding G418 resistance the fusion PCR technique was used.

Using plasmid pPRGDH6 the GAPDH promoter could be amplified by standard PCR protocols ("Experimental").

In the PCR mix pPRGDH6 and oligo's No. 5177 and 5126 (Sequences in "Experimental") were used. A 416 bp DNA fragment was generated containing the entire GAPDH promoter sequence. In addition this fragment also contains a *HindIII*, *XhoI* and a *KpnI* restriction site at its 5' end and 12 nt overlap with the 5' end of the gene encoding G418 resistance.

The 217 bp portion of the 5' end of the G418 coding sequence was also amplified by PCR using pUC-G418 and oligo's 4206 and 5127. A 226 bp DNA fragment was obtained containing the 217 bp 5' end of G418 and having a 9 nucleotides overlap with the 3' end of the earlier generated GAPDH promoter fragment. It also contained a *MscI* site at its 3 end.

The PCR fragments were purified from the PCR mixture using the WIZARD Kit. Approximately 1 µg of the GAPDH promoter fragment and 1 µg of the G418 PCR fragment were used together with oligo's 5177 and 4206 in a fusion PCR experiment (Experimental). A 621 bp DNA fragment was generated, containing the GAPDH promoter directly fused to the 5' portion of G418. After purification the DNA fragment was digested with *MscI* and *KpnI*. The 3.4 Kb *MscI*-*KpnI* fragment of pUC-G418, containing pUC sequences and the 3' portion of G418, was used as a vector.

The ligation mixture was transformed to competent *E. coli* DH5α cells. Transformant colonies containing the fusion PCR DNA inserted were identified by digestion with different restriction enzymes.

Thus, plasmid pPR1 was obtained, containing the GAPDH promoter directly fused to the G418 marker gene. Three pPR1 vectors isolated from independent transformants were used in further cloning experiments.

To target the plasmid, after transformation, to a specific integration site a 3.0-kb *SstI* fragment containing a part of the ribosomal DNA of *Phaffia* was cloned in pPR1. The ribosomal DNA fragment was isolated from an agarose gel after digestion with *SstI* of plasmid pGB-Ph11 (EP 590 707 A1). This

fragment was ligated in the dephosphorylated SstI site of pPR1. The ligation mixture was transformed to competent *E. coli* cells. Plasmid DNA was isolated and using restriction analysis it was shown that several colonies contain the expected plasmid pPR2. The complete cloning strategy is shown in Fig. 3.

### Example 6

#### Transformation of *Phaffia* with pPR2.

Transformation of *Phaffia* strain 6938 was performed using an electroporation procedure as previously described by Faber et al. (1994, Curr. Genet. 1994: 25,305-310) with the following modifications:

- Electropulsing was performed using the Bio-rad Gene Pulser with Pulse Controller and with Bio-rad 2mm cuvettes.
- *Phaffia* was cultivated for 16 h at 21 °C.
- Per transformation  $2 \times 10^8$  cells were used together with 5 µg of linearized vector. Linearization was done in the rDNA sequence using *Clal* to enable integration at the rDNA locus in the *Phaffia* genome.
- Following the electric pulse (7.5kV/cm, 400 Ω and 25 µF) 0.5 ml YePD medium was added to the cell/DNA mixture. The mixture was incubated for 2.5 h at 21 °C and subsequently spread on 5 selective YEDP agar plates containing 40 µg/ml G418.

As shown in Table 2 we were able to generate transformants with 115 transformants per µg DNA; the average transformation frequency was 50 transformants/µg pPR2 as judged over a number of experiments. Transformation of the closed circular form of pPR2 did not result in transformation suggesting that there is no autonomously replicating sequence present within the vector sequences. Using pPR2 a 10 to 50-fold increase in transformation frequency was found compared to a previous constructed transformation vector for *Phaffia*, called pGB-Ph9. In this latter vector a translation fusion was made between the 5' part of the actin gene of *Phaffia* and G418.

In order to analyze the level of resistance of transformants the mixture or DNA/cells was plated onto selective plates containing different amounts of G418. Although the total number of transformants decreases with the increasing amounts of G418, we were still able to obtain a considerable number of transformants (table 3).

In another experiment 30 transformants obtained under standard selection conditions (40 µg/ml) were transferred to plates containing 50, 200 or 1000 µg/ml. After incubation of the plates at 21 °C for 4-5 days, 23 transformants out of 30 tested were able to grow on plates containing 200 µg/ml G418. One transformant was able to grow on plates containing upto and above 1000 µg/ml G418.

Table 2. Transformation frequency of pGB-Ph9 and pPR2.

	Exp.1	Exp.2
--	69	8
pGB-Ph9xBg/II	46	7
pPR2 ccc	n.d	n.d
pPR2(A)x <i>Clal</i>	714	56
(B)	639	124

(C) 443 153

5 Total number of transformants (> 1 mm) in different transformation experiments after 4-5 days incubation.

**Table 3.** Comparison of G418 sensitivity as a result of two different G418-resistance genes in pGB-Ph9 and pPR2

concentration G418 (µg/ml)	Number of transformants	
	pPR2xClal	pGB-Ph9xBglII (=pYac4)
40	480	2
50	346	-
60	155	-
70	61	-
80	141	-
90	72	-
100	64	-

Analysis of pPR2 transformants.

25 To analyse the integration event and the number of integrated vector copies total genomic DNA from six independent transformants was isolated. Therefore these transformants were cultivated under selective conditions, i.e. YePD + 50 µg/ml G418. Chromosomal DNA was digested with *Clal*. The DNA fragments were separated by gel electrophoresis and transferred to nitrocellulose and the Southern blot was probed with *Phaffia* DNA.

30 Besides the rDNA band of 9.1 kb an additional band of 7.1 kb of similar fluorescing intensity was observed in the transformants. This band corresponds to the linearised form of pPR2. From the intensity of these bands it was concluded that the copy number was about 100 - 140 copies of pPR2. These results are similar to those observed for pGB-Ph9, ruling out that the improved G418-resistance is due to differences in copy number of integrated vectors alone. It is not known whether the multiple copy event is caused by multiple copy integration of pPR2 or by the amplification of a single copy in the  
35 rDNA or a combination of both events.

Example 7

Construction of pPR2T by cloning the GAPDH-terminator into pPR2

40 Eukaryotic mRNAs contain modified terminal sequences, specifically the 3' terminal poly(A). As the prokaryotic gene encoding G418 resistance lacks eukaryotic termination signals, which might effect proper transcription termination and mRNA stability (1994, Raue, H.A., TIBTECH 12: 444-449), a part of the 3' non-coding sequence of GAPDH was introduced.

To that end, a 307 bp fragment, consisting of 281 bp of the 3' non-coding region of GAPDH and other additional cloning sequences, was amplified by PCR using the oligo's 5137 and 5138 ("Experimental").  
45 The upstream oligo 5137 consists of the last 14 nucleotides of the coding and 17 nucleotides of the 3' non-coding region of GAPDH. By base substitutions of the 5th (T --> A) and 8th (T --> C) nucleotide

of the non-coding sequence a *Bam*HI restriction site was introduced. In addition this fragment contains a *Xho*I and a *Hind*III restriction site at its 3' end.

The PCR fragment was purified from the PCR mixture using the WIZARD Purification Kit and digested with *Bam*HI and *Hind*III. A 288 bp fragment was isolated and cloned into the corresponding sites of the previously constructed *Phaffia* transformation vector pPR2, yielding pPR2T.

Upon transformation of *Phaffia*, using G418 as selective agent, the transformation frequencies (number of transformants per  $\mu$ g of DNA) obtained with the improved construct pPR2T was approximately 5 to 10 times higher than the transformation frequency of pPR2 (i.e. without a *Phaffia* homologous transcription termination signal). The results of a typical experiment are given in Table 4.

**Table 4 Transformation frequency at 50  $\mu$ g/ml G418 for pGB-Ph9, pPR2 and pPR2T**

Vector	transformants	transformants/ $\mu$ g DNA
pGB-Ph9 (ccc)	-	-
pGB-Ph9 (xBglII)	60	1
pPR2 (ccc)	1	-
pPR2 (xClal)	3000 - 9600	50 - 160
pPR2T (ccc)	-	-
pPR2T (xClal)	45600	760
pPR2T (xSfiI)	1080	18

*Phaffia* cells transformed with pPR2T were tested for their ability to grow on high levels of G418. The level of G418 on which growth is still possible was taken as a measure of the expression level of the G418 resistance gene in transformants, as a result of the presence of the *Phaffia* promoter, and/or terminator. Preliminary results indicate that the number of transformants able to grow on high levels of G418 are significantly higher than without terminator.

#### In summary

From the above results, it was concluded, that the presence of the GAPDH-promoter (pPR2) resulted in a considerable increase of the transformation frequency (from 1 to at least 50 per  $\mu$ g of DNA) when compared to the vector containing the actin-promoter (pGB-Ph9). These results are in line with the results obtained with the G418 sensitivity test (Table 3 and 4) which indicate superior expression levels under the control of the GAPDH promoter. The possibility that the difference in transformation frequency could be due solely to the difference in linearising the vectors, (*Bgl*II, *Clal* and *Sfi*I all cut inside the ribosomal DNA locus, but at different positions), was ruled out by comparison of pPR2(x*Sfi*I) with pGB-Ph9(x*Sfi*I). The difference in transformation frequency between the two pPR2 and pGB-Ph9, linearised with *Sfi*I is still considerable. However, it is concluded that the choice of the linearisation site does have effect on the transformation frequency; linearisation with *Clal* is preferred.

The improvements obtained by using a high-level promoter, such as GAPDH, are irrespective of whether a homologous terminator is used (pPR2 (without homologous terminator) performs far better than pGB-Ph9, both in G418 sensitivity tests, as well as in terms of transformation frequency).

The presence of a homologous terminator results in both higher transformation frequencies and higher expression levels; this result is concluded to be independent of the promoter used. Preliminary results indicate that considerable improvements are obtained when the pGB-Ph9 construct is completed with a transcription terminator, such as the GAPDH-terminator used in pPR2T.

The following Examples illustrate the isolation of DNA encoding enzymes involved in the carotenoid biosynthesis pathway of *Phaffia rhodozyma*. These DNA sequences can suitably be used for a variety of purposes; for example to detect and isolate DNA sequences encoding similar enzymes in other organisms, such as yeast by routine hybridisation procedures, to isolate the transcription promoters and/or terminators, which can be used to construct expression vectors for both heterologous as well as homologous downstream sequences to be expressed. The DNA sequences encoding carotenoid biosynthesis genes can suitably be used to study the over-expression, either under the control of their own promoters or heterologous promoters, such as the glycolytic pathway promoters illustrated above. For example, transformation of *Phaffia rhodozyma* with carotenoid encoding DNA sequences according to the invention effectively results in amplification of the gene with respect to the wild-type situation, and as a consequence thereof to overexpression of the encoded enzyme.

Hence, the effect of over-expression of one or more genes encoding carotenoid biosynthesis genes can thus be studied. It is envisaged that mutant *Phaffia* strains can be obtained producing higher amounts of valuable carotenoids, such as  $\beta$ -carotene, cantaxanthin, zeaxanthin and/or astaxanthin. Similarly, the DNA sequences encoding enzymes involved in the carotenoid biosynthesis pathway can be introduced into other hosts, such as bacteria, for example *E. coli*, yeasts, for example species of *Saccharomyces*, *Kluyveromyces*, *Rhodospiridium*, *Candida*, *Yarrowia*, *Phycomyces*, *Hansenula*, *Picchia*, fungi, such as *Aspergillus*, *Fusarium*, and plants such as carrot, tomato, and the like. The procedures of transformation and expression requirements are well known to persons skilled in these arts.

Strains: *E. coli* XL-Blue-MRF' $\Delta$ (*mcrA*)183 $\Delta$ (*mcrCB-hsdSMR-mrr*) 173 *endA*1 *supE*44 *thi*-1 *recA*1 *gyrA*96 *relA*1 *lac*[F' *proAB* *laq*<sup>+</sup>Z $\Delta$ M15 Tn10 (Tet<sup>r</sup>)]

ExAssist<sup>TM</sup> interference-resistant helper phage (Stratagene<sup>R</sup>)

*P. rhodozyma* CBS6938 or

*P. rhodozyma* asta 1043-3

Plasmids used for cloning:

pUC19 Ap<sup>r</sup> (Gibco BRL)

Uni-ZAP<sup>TM</sup> XR vector (lambda ZAP<sup>R</sup> II vector digested with *Eco*RI-*Xho*I, CIAP treated; Stratagene<sup>R</sup>)

Media: LB: 10 g/l bacto tryptone, 5 g/l yeast extract, 10 g/l NaCl. Plates; +20 g/l bacto agar.

When appropriate 50-100 µg/ml ampicillin (Ap), 30 µg/ml chloramphenicol (Cm) and 1 mM isopropyl-1-thio-β-D-galactopyranoside (IPTG) was added.

YePD: 10 g/l yeast extract, 20 g/l bacto peptone, 20 g/l glucose. Plates; +20 g/l bacto agar.

All molecular cloning techniques were essentially carried out as described by Sambrook et al. in Molecular Cloning: a Laboratory Manual, 2nd Edition (1989; Cold Spring Harbor Laboratory Press). Transformation of *E. coli* was performed according to the CaCl<sub>2</sub> method described by Sambrook *et al.*

Enzyme incubations were performed following instructions described by the manufacturer. These incubations include restriction enzyme digestion, dephosphorylation and ligation (Gibco BRL).

Isolation of plasmid DNA from *E. coli* was performed using the QIAGEN (Westburg B.V. NL).

For sequence analysis deletions constructs and oligonucleotides were made to sequence the complete sequence using a Taq DYE Primer Cycle Sequencing kit (Applied Biosystems).

### Example 8

#### Description of plasmids

Plasmids (pACCAR25ΔcrtE, pACCAR25ΔcrtB, pACCRT-E1B, pACCAR16ΔcrtX and pACCAR25ΔcrtX), which contain different combinations of genes involved in the biosynthesis of carotenoid in *Erwinia uredovora* were gifts from Prof. Misawa; Kirin Brewery co., LTD.; Japan). The biosynthetic route of carotenoid synthesis in *Erwinia uredovora* is shown in fig 8.

In addition a derivative of pACCAR25ΔcrtX, designated pACCAR25ΔcrtXΔcrtI, was made in our laboratory. By the introduction of a frameshift in the *Bam*HI restriction site the crtI gene was inactivated. *E. coli* strains harboring this plasmid accumulate phytoene which can be monitored by the red phenotype of the colony.

All plasmids are derivatives of plasmid pACYC184 (Rose RE; Nucl. Acids Res. 16 (1988) 355), which contains a marker conferring chloramphenicol-resistance. Furthermore these plasmids and derivatives thereof contain a replication origin that is compatible to vectors such as pUC and pBluescript. Each plasmid contains a set of carotenoid biosynthetic genes of *Erwinia uredovora* mediating the formation of different carotenoid in *E. coli*. The complete list of plasmid used in this study is shown in Table 5.

Table 5: Summary of carotenoid producing *E. coli* strains used in this study.

PLASMID:	GENOTYPE:	CAROTENOID ACCUMULATED:	COLOR PHENOTYPE:
pACCAR25ΔcrtE	<i>crtB; crtI; crtY;</i> <i>crtX;</i> <i>crtZ</i>	farnesyl pyrophosphate/iso-pentenyl pyrophosphate	white
pACCAR25ΔcrtB	<i>crtE; crtI; crtY;</i> <i>crtX;</i> <i>crtZ</i>	geranylgeranyl pyrophosphate	white
pACCAR25ΔcrtX ΔcrtI	<i>crtE; crtB; crtY;</i> <i>crtZ</i>	phytoene	white

pACCRT-EIB	<i>crtE; crtB; crtI</i>	lycopene	red
pACCAR16Δ <i>crtX</i>	<i>crtE; crtB; crtI</i> <i>crtY</i>	β-carotene	yellow
pACCAR25Δ <i>crtX</i>	<i>crtE; crtB; crtI</i> ; <i>crtY</i> ; <i>crtZ</i>	zeaxanthin	yellow/ orange

Genes encoding: *crtE*, geranylgeranyl pyrophosphate synthase; *crtB*, Phytoene synthase; *crtI*, phytoene desaturase; *crtY*, lycopene cyclase; *crtX*, β-carotene hydroxylase; *crtZ*, zeaxanthin glycosylase

#### Example 9

##### Construction of cDNA library of *Phaffia rhodozyma*

##### a) Isolation of total RNA from *Phaffia rhodozyma*

All solutions were made in DEPC-treated distilled water and all equipments were soaked overnight in 0.1% DEPC and then autoclaved.

A 300 ml Erlenmeyer containing 60 ml YePD culture medium was inoculated with *Phaffia rhodozyma* strain CBS6938/1043-3 from a preculture to a final OD<sub>600</sub> of 0.1. This culture was incubated at 21 °C (300 rpm) until the OD<sub>600</sub> had reached 3-4.

The cells were harvest by centrifugation (4 °C, 8000 rpm, 5 min) and were resuspended in 12 ml of ice-cold extraction-buffer (0.1 M Tris-HCl, pH 7.5; 0.1 M LiCl; 0.1 mM EDTA). After centrifugation cells were resuspended in 2 ml of ice-cold extraction-buffer, 4 g of glassbeads (0.25 mm) and 2 ml phenol were added.

The mixture was vortexed 5 times at maximum speed for 30 s with 30 s cooling incubation intervals on ice.

The cell/glassbeads/phenol mixture was centrifuged (5 min, 15.300 rpm , 4 °C) and the aqueous phase (sup 1) was transferred to a fresh tube and was kept on ice.

The phenolic phase was retracted by adding an additional volume of 1 ml extraction buffer and 2 ml phenol.

After centrifugation (5 min, 15.300 rpm , 4 °C). the aquaous phase was transferred to sup 1 and extracted with an equal volume phenol:chloroform.

After centrifugation (5 min, 15.300 rpm , 4 °C), the aquaous phase was transferred to a fresh tube and 0.1 volume of 3 M NaAc; pH5.5 and 2.5 volumes of EtOH was added to precipitate RNA (incubation overnight -20 °C).

The precipitate was collected by centrifugation (10 min, 15.300 rpm , 4 °C) and drained off excess liquid and the RNA pellet was washed with 70 % icecold EtOH.



After removing excess liquid the RNA was resuspended in 200 - 800 µl DEPC-treated water. RNA was stored at -70 °C. A 60 ml culture yielded 400 - 1500 µg total RNA. The integrity of total RNA was checked by formaldehyde RNA gel electrophoresis.

5    b) Selection of poly(A)<sup>+</sup> RNA

Isolation of poly(A)<sup>+</sup> from total RNA was carried out essential as described by Sambrook et al., 1989 (Molecular cloning, a laboratory manual, second edition) using the following solutions.

All solutions were prepared in DEPC-treated water and autoclaved.

10    RNA denaturation buffer:                    1 M NaCl; 18% (v/v) DMSO.

Column-loading buffer (HEND): 10 mM Hepes, pH 7.6; 1 mM EDTA; 0.5 M Na Cl; 9% (v/v) DMSO.

Elution buffer (HE):                            10 mM Hepes, pH 7.6; 1 mM    EDTA.

Oligo(dT)-cellulose Type 7 was supplied by Pharmacia Biotech. 0.1 g (dry weight) of oligo(dT)-cellulose was add to 1 ml HEND and the suspension was gently shaken for 1 h at 4 °C. Total RNA (1.5  
15    mg dissolved in 500 µl) and 1 ml 1 M NaCl; 18% (v/v) DMSO was heated to 65 °C for 5 min. Then 600 µl NaCl/DMSO was added to the RNA, mixed and placed on ice for 5 min. The poly(A)<sup>+</sup> isolation was carried out be two cycles of purification. The final yield was about 45 µg poly(A)<sup>+</sup> RNA.

c) cDNA synthesis

20

cDNAs were synthesized from 7.5 µg poly(A)<sup>+</sup>-RNAs using the cDNA Synthesis Kit (#200401; Strategene<sup>®</sup>). Synthesis was carried out according to the instruction manual with some minor modification.

SuperScript<sup>™</sup> II RNase H<sup>-</sup> Reverse Transcriptase (Gibco BRL) was used in the first strand reaction  
25    instead of MMLV-RT.

The following reagents were add in a microcentrifuge:

3 µl of poly(A)<sup>+</sup> RNAs

2 µl of linker-primer

23.5 µl DMQ

30    Incubate 10 min 70 °C, spin quickly in microcentrifuge and add,

10 µl of 5 x First Strand Buffer (provided by Gibco BRL)

5 µl of 0.1 M DTT (provided by Gibco BRL)

3 µl of first strand methyl nucleotide mixture

1 µl of RNase Block Ribonuclease Inhibitor (40 U/µl)

35    Annealling of template and primers by incubation the mixture at 25 °C for 10 min followed by 2 min at 42 °C and finally add;

2.5 µl SuperScript<sup>™</sup> II RNase H<sup>-</sup> Reverse Transcriptase

First-strand reaction was carried out at 42 °C for 1 h.

Size fractionation was carried out using GeneClean<sup>®</sup> II kit ( supplied BIO 101, Inc.). The volume of the cDNA mixture obtained after *Xho*I digestion was brought up by adding DMQ to a final volume of 200  $\mu$ l. Three volumes of Nal was added and the microcentrifuge tube was placed on ice for 5 min. The pellet of glassmilk was washed three times using 500  $\mu$ l New Wash. Finally the cDNA was eluted in 20  $\mu$ l DMQ.

The yield of cDNA was about 1  $\mu$ g using these conditions.

#### d) cDNA cloning

cDNA library was constructed in the Uni-ZAP<sup>™</sup> XR vector using 100 ng cDNAs. Ligation was performed two times overnight incubation at 12 °C. The cDNA library was packaged using the Packagene<sup>®</sup> lambda DNA packaging system (Promega) according to the instruction manual. The calculated titer of the cDNA library was  $3.5 \cdot 10^6$  pfu.

#### e) Mass excission

Mass excision was carried out described in the protocol using derivatives of *E. coli* XL-Blue-MRF' as acceptor strain (see Table 5). Dilution of cell mixtures were plated onto 145 mm LB agar plates containing ampicillin, chloramphenicol and IPTG, yielding 250 - 7000 colonies on each plate. The plates were incubated overnight at 37 °C and further incubated one or two more days at room temperature.

### Example 10

#### Cloning of the geranylgeranyl pyrophosphate synthase gene (*crtE*) of *Phaffia rhodozyma*

##### a) Isolation of cDNA clone

The entire library was excised into a farnesylpyrophosphate/ isopentenyl pyrophosphate accumulating cells of *E. coli* XL-Blue-MRF, which carries the plasmid pACCAR25 $\Delta$ crtE (further indicated as XL-Blue-MRF'[pACCAR25 $\Delta$ crtE]). The screening for the *crtE* gene was based on the color of the transformants. Introduction of the *crtB* gene in a genetic background of XL-Blue-MRF'[pACCAR25 $\Delta$ crtE] would result in a restoration of the complete route for the biosynthesis of zeaxanthin-diglucoside, which could be monitored by the presence of a yellow/orange pigmented colony. About 8.000 colonies were spread on LB agar plates containing appropriate antibiotics and IPTG. One colony was found to have changed to a yellow/orange color.

35

##### b) Characterization of complementing cDNA clone

These colonies were streaked on LB-ampicillin agar plates. Plasmid DNA was isolated from this yellow colonies and found to include a 1.85 kb fragment (Fig 2A). The resulting plasmid, designated pPRcrtE,

Blank

was used for retransformation experiments (Table 6). Only the transformation of XL-Blue-MRF'[pACCAR25ΔcrtE] with pPRcrtE resulted in a white to yellow color change in phenotype. To test whether the color change was due to complementation and not caused by cDNA alone pPRcrtE was transformed into XL-Blue-MRF'. Selection of transformants on LB-ampicillin agar plate containing IPTG did not result in color changes of the colonies (Table 6). Therefore we tentatively concluded, that we have cloned a cDNA of *P. rhodozyma* encoding GPPP synthase which is involved in the conversion of IPP and FPP to GGPP.

Table 6: Color phenotype of carotenoid producing *E. coli* strains transformed with pPRcrtE.

	pUC19 (control)	pPRcrtE
XL-Blue-MRF' (Ap, IPTG)	white	white
XL-Blue-MRF' [pACCAR25ΔcrtE] (Ap, Cm, IPTG)	white	yellow/orange
XL-Blue-MRF' [pACCAR25ΔcrtB] (Ap, Cm, IPTG)	white	white

Transformation: 10 ng of each plasmid was mixed to CaCl<sub>2</sub> competent *E. coli* cells. Transformant cells were selected by plating 1/10 and 1/100 volume of the DNA/cell mixture on LB agar-medium containing the appropriate antibiotics (in brackets).

#### c) Sequence analysis of cDNA fragment

Plasmid pPRcrtE was used to determine the nucleotide sequence of the 1.85 kb cDNA.

The sequence comprised 1830 nucleotides and a 31 bp poly(A) tail. An open reading frame (ORF) of 375 amino acids was predicted. The nucleotide sequence and deduced amino acid sequence are shown as SEQIDNO: NO 14 and 15, respectively. A search in SWISS-PROT protein sequence data bases using the Blitz amino acid sequence alignment program indicated amino acid homology (52 % in 132 aa overlap; *Neurospora crassa*) especially to the conserved domain I in geranylgeranyl-PPI synthase enzymes of different organisms (Botella et al., Eur. J. Biochem. (1995) 233; 238-248).

#### Example 11

##### Cloning of the phytoene synthase gene (*crtB*) of *Phaffia rhodozyma*

#### a) Isolation of cDNA clone

The entire library was excised into a geranylgeranylpyrophosphate accumulating cells of *E. coli* XL-Blue-MRF', which carries the plasmid pACCAR25ΔcrtB (further indicated as XL-Blue-MRF'[pACCAR25ΔcrtB]). The screening for the *crtB* gene was based on the color of the transformants.

Introduction of the *crtB* gene in a genetic background of XL-Blue-MRF'[pACCAR25Δ*crtB*] would result in a restoration of the complete route for the biosynthesis of zeaxanthin-diglucoside, which could be monitored by the presence of a yellow/orange pigmented colony.

About 25.000 colonies were incubated on LB agar plates containing appropriate antibiotics and IPTG.

5 Three colonies were found to have changed to a yellow/orange color.

#### b) Characterization of complementing cDNA clone

These colonies were streaked on LB-ampicillin agar plates. Plasmid DNA, designated pPRcrtB1 to 3, was isolated from these yellow colonies and found to include a 2.5 kb fragment (Fig 2B). One of the resulting plasmids, pPRcrtB1 was used for retransformation experiments (Table 7). Only the transformation of XL-Blue-MRF'[pACCAR25Δ*crtB*] with pPRcrtB resulted in a white to yellow color change in phenotype. Therefore we tentative conclude that we have cloned a cDNA of *P. rhodozyma* encoding phytoene synthase which is involved in the conversion of 2 GGPP molecules via prephytoene pyrophosphate into phytoene.

Table 7: Color phenotype of carotenoid producing *E. coli* strains transformed with pPRcrtB.

	pUC19 (control)	pPRcrtB
20 XL-Blue-MRF' (Ap, IPTG)	white	white
XL-Blue-MRF' [pACCAR25Δ <i>crtB</i> (Ap, Cm, IPTG)	white	yellow/orange
25 XL-Blue-MRF' [pACCAR25Δ <i>crtE</i> (Ap, Cm, IPTG)	white	white

Legend: see Table 6.

#### c) Sequence analysis of cDNA fragment.

Plasmid pPRcrtB2, which contains the longest cDNA insert, was used to determine the nucleotide sequence of the 2.5 kb cDNA. The sequence comprised 2483 nucleotides and a 20 bp poly(A) tail. An open reading frame (ORF) of 684 amino acids was predicted. The nucleotide sequence and deduced amino acid sequence are shown in SEQIDNOs: 12 and 13, respectively. A search in SWISS-PROT protein sequence data bases using the Blitz amino acid sequence alignment program Data indicated some amino acid homology (26 % identity in 441 aa overlap of *crtB* gene of *Neurospora crassa*) with *crtB* genes of other organisms.

#### Example 12

Cloning of the phytoene desaturase gene (*crtI*) of *Phaffia rhodozyma*

a) Isolation of cDNA clone

The entire library was excised into a phytoene accumulating cells of *E.coli* XL-Blue-MRF', which carries the plasmid pACCAR25 $\Delta$ crtX $\Delta$ crtI (further indicated as XL-Blue-MRF'[pACCAR25 $\Delta$ crtX $\Delta$ crtI]). The screening for the *crtI* gene was based on the color of the transformants. Introduction of the *crtI* gene in a genetic background of XL-Blue-MRF'[pACCAR25 $\Delta$ crtX $\Delta$ crtI] would result in a restoration of the complete route for the biosynthesis of zeaxanthin, which could be monitored by the presence of a yellow/orange pigmented colony.

About 14.000 colonies were incubated on LB agar plates containing appropriate antibiotics and IPTG. Two colonies were found to have changed to a yellow/orange color.

b) Characterization of complementing cDNA clones

These colonies were streaked on LB-ampicillin agar plates. Plasmid DNA, designated pPRcrtI.1 and pPRcrtI.2, was isolated from these yellow colonies and found to include a 2.0 kb fragment (Fig 2C).

One of the resulting plasmids, pPRcrtI.1 was used for retransformation experiments (Table 8). Only the transformation of XL-Blue-MRF'[pACCAR25 $\Delta$ crtX $\Delta$ crtI] with pPRcrtI resulted in a white to yellow color change in phenotype. Therefore we tentative conclude that we have cloned a cDNA of *P. rhodozyma* encoding phytoene desaturase which is involved in the conversion of phytoene to lycopene.

Table 8: Color phenotype of carotenoid producing *E. coli* strains transformed with pPRcrtI.

	pUC19	pPRcrtI
XL-Blue-MRF' (Ap, IPTG)	white	white
XL-Blue-MRF' [pACCAR25 $\Delta$ crtX $\Delta$ crtI (Ap, Cm, IPTG)	white	yellow/orange
XL-Blue-MRF' [pACCAR25 $\Delta$ crtB (Ap, Cm, IPTG)	white	white

Legend: see Table 6.

c) Sequence analysis of cDNA fragment

One of the plasmid pPRcrtI was used to determine the nucleotide sequence of the 2.0 kb cDNA. The sequence comprised 2038 nucleotides and a 20 bp poly(A) tail. An open reading frame (ORF) of 582 amino acids was predicted. The nucleotide sequence and deduced amino acid sequence are shown in SEQIDNOs: 16 and 17, respectively. A search in SWISS-PROT protein sequence data bases using the Blitz amino acid sequence alignment program Data indicated amino acid homology to phytoene desaturase gene of *N. crassa* (53% identity in 529 aa overlap).

Example 13Cloning of the lycopene cyclase gene (*crtY*) of *Phaffia rhodozyma*a) Isolation of cDNA clone

- 5 The entire library was excised into a lycopene accumulating cells of *E. coli* XL-Blue-MRF', which carries the plasmid pACCRT-EIB (further indicated as XL-Blue-MRF'[pACCRT-EIB]). The screening for the *crtY* gene was based on the color of the transformants. Introduction of the *crtY* gene in a genetic background of XL-Blue-MRF'[pACCRT-EIB] would result in a restoration of the complete route for the biosynthesis of  $\beta$ -carotene, which could be monitored by the presence of a yellow pigmented colony.
- 10 About 8.000 colonies were incubated on LB agar plates containing appropriate antibiotics and IPTG. One colony was found to have changed to a yellow color.

b) Characterization of complementing cDNA clone

- 15 This colony was streaked on LB-ampicillin agar plates. Plasmid DNA was isolated from this yellow colony and found to include a 2.5 kb fragment (Fig 2B). The resulting plasmid, designated pPRcrtY, was used for retransformation experiments (Table 9. Surprisingly, not only transformation of XL-Blue-MRF'[pACCRT-EIB] but also transformation of XL-Blue-MRF'[pACCAR25 $\Delta$ crtB] with pPRcrtY resulted in a red to yellow color change in phenotype.

20 Table 9: Color phenotype of carotenoid producing *E. coli* strains transformed with pPRcrtY.

	pUC19	pPRcrtB
XL-Blue-MRF' (Ap, IPTG)	white	white
25 XL-Blue-MRF' [pACCRT-EIB (Ap, Cm, IPTG)	red	yellow
30 XL-Blue-MRF' [pACCAR25 $\Delta$ crtB (Ap, Cm, IPTG)	red	yellow

Legend: see Table 6.

- A second transformation experiment was carried out including the previously cloned cDNA of pPRcrtB.
- 35 As shown in table 6 the cDNA previously (example 3) isolated as encoding phytoene synthase was able to complement the *crtY* deletion resulting in the biosynthesis of  $\beta$ -carotene in XL-Blue-MRF'[pACCRT-EIB].

Sequence analysis of the cDNA insert of pPRcrtY (SEQIDNOs: 18 and 19) showed that it was similar to the sequence of cDNA fragment of pPRcrtB.

From these data we tentatively conclude that we have cloned a cDNA of *P. rhodozyma* encoding phytoene synthase and lycopene cyclase which is involved in the conversion of 2 GGPP molecules via prephytoene pyrophosphate into phytoene and lycopene to  $\beta$ -carotene, respectively. This is the first gene in a biosynthetic pathway of carotenoids synthesis that encodes two enzymatic activities.

Table 10: Color phenotype of carotenoid producing *E. coli* strains transformed with different cDNAs of *Phaffia rhodozyma* (Ap, Cm, IPTG).

	pUC19	pPRcrtE	pPRcrtB	pPRcrtY
XL-Blue-MRF' [pACCAR25 $\Delta$ crtE]	white	yellow/ orange	white	white
XL-Blue-MRF' [pACCAR25 $\Delta$ crtB]	white	white	yellow/ orange	yellow/ orange
XL-Blue-MRF' [pACCRT-EIB]	red	red	yellow	yellow

Legend: see Table 6

#### Example 14

##### Cloning of the isopentenyl diphosphate (IPP) isomerase gene (*idi*) of *Phaffia rhodozyma*

##### a) Isolation of cDNA clone

The entire *Phaffia* cDNA library was excised into lycopene accumulating cells of *E. coli* XL-Blue-MRF', each carrying the plasmid pACCRT-EIB (further indicated as XL-Blue-MRF'[pACCRT-EIB]).

About 15.000 colonies were incubated on LB agar plates containing appropriate antibiotics and IPTG. One colony was found to have a dark red colour phenotype.

##### b) Characterization of complementing cDNA clone

This colony was streaked on LB-ampicillin agar plates. Plasmid DNA was isolated from this yellow colony and found to include a 1.1 kb fragment. The resulting plasmid, designated pPRcrtX, was used for retransformation experiments (Table 11).

All colonies of XL-Blue-MRF'[pACCAR-EIB] transformed with pPRcrtX had a dark red phenotype. From these data we tentatively concluded, that we have cloned a cDNA of *P. rhodozyma* expression of which results in an increased lycopene production in a genetically engineered *E. coli* strain.

Table 11: Color phenotype of carotenoid producing *E. coli* strains transformed with pPRcrtX.



	pUC19	pPRcrtX
XL-Blue-MRF' (Ap, IPTG)	white	white
XL-Blue-MRF' [pACCRT-EIB (Ap, Cm, IPTG)	red	dark red

Legend: see Table 6.

#### c) Sequence analysis of cDNA fragment

In order to resolve the nature of this gene the complete nucleotide sequence of the cDNA insert in pPRcrtX was determined. The nucleotide sequence consist of the 1144 bp. The sequence comprised 1126 nucleotides and a poly(A) tail of 18 nucleotides. An open reading frame (ORF) of 251 aminoacids with a molecular mass of 28.7 kDa was predicted. The nucleotide sequence and deduced amino acid sequence are shown in SEQIDNOs: 20 and 21, respectively.

A search in SWISS-PROT protein sequence data bases using the Blitz amino acid sequence alignment program Data indicated aminoacid homology to isopentenylidiphosphate (IPP) isomerase (*idi*) of *S. cerevisiae* (42.2 % identity in 200 aminoacid overlap). IPP isomerase catalyzes an essential activation step in the isoprene biosynthetic pathway which synthesis the 5-carbon building block of carotenoids. In analogy to yeast the gene of *Phaffia* was called *idi1*. The cDNA clone carrying the genes was then called pPR*idi*.

#### Example 15

##### Overexpression of the *idi* gene of *P. rhodozyma* in a carotenogenic *E. coli*

Lycopene accumulating cells of *E.coli* XL-Blue-MRF', which carry the plasmid pACCRT-EIB (further indicated as XL-Blue-MRF'[pACCRT-EIB]) were transformed with pUC19 and pPR*idi* and transformants were selected on solidified LB-medium containing Amp and Cm. The transformants, called XL-Blue-MRF'[pACCRT-EIB/pUC19 and [pACCRT-EIB/pPR*idi*], were cultivated in 30 ml LB-medium containing Amp, Cm and IPTG at 37 °C at 250 rpm for 16 h. From these cultures 1 ml was used for carotenoid extraction and analysis. After centrifugation the cell pellet was dissolved in 200 µl acetone and incubated at 65 °C for 30 minutes. Fifty µl of the cell-free acetone fraction was then used for high-performance liquid chromatography (HPLC) analysis. The column (chrompack cat. 28265; packing nucleosil 100C18) was developed with water-acetonitrile-2-propanol (from 0 to 45 minutes 9:10:81 and after 45 minutes 2:18:80) at a flow rate of 0.4 ml per minute and recorded with a photodiode array detector at 470 +/- 20 nm. Lycopene was shown to have a retention time of about 23 minutes under these conditions. The peak area was used as the relative lycopene production (mAu\*s). The relative

lycopene production was 395 and 1165 for XL-Blue-MRF'[pACCRT-EIB/pUC19] and [pACCRT-EIB/pPR*idi*], respectively.

These data show the potentials of metabolic pathway engineering in *Phaffia*, as increased expression of the *idi* of *Phaffia rhodozyma* causes a 3-fold increase in carotenoid biosynthesis in *E. coli*.

This cDNA may be over-expressed in a transformed *Phaffia* cell with a view to enhance carotenoid and/or xanthophyll levels. The cDNA is suitably cloned under the control of a promoter active in *Phaffia*, such as a strong promoter according to his invention, for example a *Phaffia* glycolytic pathway promoter, such as the GAPDH-gene promoter disclosed herein, or a *Phaffia* ribosomal protein gene promoter according to the invention (*vide sub*). Optionally, the cDNA is cloned in front of a transcriptional terminator and/or polyadenylation site according to the invention, such as the GAPDH-gene terminator/polyadenylation site. The feasibility of this approach is illustrated in the next example, where the *crtB* gene from *Erwinia uredovora* is over-expressed in *Phaffia rhodozyma* by way of illustration.

#### Example 16

##### Heterologous expression of carotenogenic gene from *Erwinia uredovora* in *Phaffia rhodozyma*.

The coding sequence encoding phytoene synthase (*crtB*) of *Erwinia uredovora* (Misawa et al., 1990) was cloned between the promoter and terminator sequences of the *gpd* (GAPDH-gene) of *Phaffia* by fusion PCR. In two separate PCR reactions the promoter sequence of *gpd* and the coding sequence of *crtB* were amplified. The former sequence was amplified using the primers 5177 and 5128 and pPR8 as template. This latter vector is a derivative of the *Phaffia* transformation vector pPR2 in which the promoter sequence has been enlarged and the *Bgl*II restriction site has been removed. The promoter sequence of *gpd* was amplified by PCR using the primers 5226 and 5307 and plasmid pPRgpd6 as template. The amplified promoter fragment was isolated, digested with *Kpn*I and *Bam*HI and cloned in the *Kpn*I-*Bgl*II fragment of vector pPR2, yielding pPR8. The coding sequence of *crtB* was amplified using the primers 5131 and 5134 and pACCRT-EIB as template. In a second fusion PCR reaction, using the primers 5177 and 5134, 1 µg of the amplified promoter and *crtB* coding region fragment used as template yielding the fusion product *Pgpd-crtB*. The terminator sequence was amplified under standard PCR conditions using the primers 5137 and 5138 and the plasmid pPRgdh6 as template. Primer 5137 contains at the 5' end the last 11 nucleotides of the coding region of the *crtB* gene of *E. uredovora* and the first 16 nucleotides of the terminator sequence of *gpd* gene of *P. rhodozyma*. By a two basepair substitution a *Bam*HI restriction site was introduced. The amplified fusion product (*Pgpd-crtB*) and the amplified terminator fragments were purified and digested with *Hind*III and *Bam*HI and cloned in the dephosphorylated *Hind*III site of the cloning vector pMTL25. The vector with the construct *Pgpd-crtB-Tgpd* was named pPREX1.1.

The *Hind*III fragment containing the expression cassette *Pgpd-crtB-Tgpd* was isolated from pPREX1.1 and ligated in the dephosphorylated *Hind*III site of the *Phaffia* transformation vector pPR8. After transformation of the ligation mixture into *E. coli* a vector (pPR8*crtB*6.1) with the correct insert was chosen for *Phaffia* transformation experiments.

*Phaffia* strain CBS6938 was transformed with pPR8*crtB*6.1, carrying the expression cassette P*gpd*-*crtB*-T*gpd*, and transformants were selected on plates containing G418. The relative amount of astaxanthin per OD<sub>660</sub> in three G418-resistant transformants and the wild-type *Phaffia* strains was determined by HPLC analysis (Table 12). For carotenoid isolation from *Phaffia* the method of DMSO/hexane extraction described by Sedmak *et al.*, (1990; *Biotechn. Techniq.* 4, 107-112) was used.

Table 12. The relative astaxanthin production in a *Phaffia* transformant carrying the *crtB* gene of *E. uredoovora*.

Relative amount	of astaxanthin
Strain:	(mAU*s/OD <sub>660</sub> )
<i>P. rhodozyma</i> CBS6938	448
<i>P. rhodozyma</i> CBS6938	
[pPR8 <i>crtB</i> 6.1]#1	626
[pPR8 <i>crtB</i> 6.1]#2	716
[pPR8 <i>crtB</i> 6.1]#4	726
Primers used:	

5128: 5' *caactgccatgatggttaagagtgttagag* 3'

5177: 5' *cccaagctttctcgaggtacctgggtgggtcatgtatgtac* 3'

5131: 5' *taccatcatggcagttggctcgaaaag* 3'

5134: 5' *cccaagcttgcgtcgtctagagcggcgctgcc* 3'

5137: 5' *ccaagcctaaccggatccctccaaacc* 3'

5138: 5' *gccaaagcttctcgagcttgatcagataaagatagagat* 3'

5307: 5' *gttgaagaaggatccttggatga* 3'

The *gpd* sequences are indicated in bold, the *crtB* sequences in italic, additional restriction sites for cloning are underlined and base substitution are indicated by double underlining.

#### Example 17

##### Isolation and characterization of the *crtB* gene of *Phaffia*

It will also be possible to express the *Phaffia rhodozyma* gene corresponding to *crtB* and express it under the control of its own regulatory regions, or under the control of a promoter of a highly expressed gene according to the invention. The *Phaffia* transformation procedure disclosed herein, invariably leads to stably integrated high copy numbers of the introduced DNA, and it is expected, that expression of the gene under the control of its own promoter will also lead to enhanced production of

carotenoids, including astaxanthin. To illustrate the principle, a protocol is given for the cloning of the *crtB* genomic sequence, below.

To obtain the genomic *crtB*-gene including expression signals the 2.5 kb *Bam*HI-*Xho*I fragment was isolated from the vector pPRcrtB and used as probe to screen a cosmid library of *Phaffia*.

5 The construction and screening of the library was carried out as described in Example 3 using the *crtB* gene as probe instead of the *gapdh*-gene.

After the rounds of hybridization, 2 colonies were identified giving a strong hybridization signal on the autoradiogram after exposure. Cosmid DNA isolated from these colonies was called pPRgcrB#1.1 and pPRgcrB#7, respectively.

10 Chromosomal DNA isolated from *Phaffia rhodozyma* strain CBS 6938 and cosmid pPRgcrB#7 was digested with several restriction enzymes. The DNA fragments were separated, blotted and hybridized with a amino-terminal specific probe (0.45 kb *Xba*I fragment) of *crtB* under conditions as described before. After exposure, the autoradiogram showed DNA fragments of different length digested by different restriction enzymes which hybridized with the *crtB* probe. On the basis that no *Eco*RI site is  
15 present in the cDNA clone a *Eco*RI fragment of about 4.5 kb was chosen for subcloning experiments in order to determine the sequence in the promoter region and to establish the presence of intron sequences in the *crtB* gene. A similar sized hybridizing fragment was also found in the chromosomal DNA digested with *Eco*RI. The fragment was isolated from an agarose gel and ligated into the corresponding site of pUC19. The ligation mixture was transformed to competent *E. coli* cells. Plasmids with the correct insert  
20 in both orientations, named pPR10.1 and pPR10.2, were isolated from the transformants. Comparison of the restriction patterns of pPR10.1/pPR10.2 and pPRcrtB digested with *Xba*I gave an indication for the presence of one or more introns as the internal 2.0 kb *Xba*I fragment in the cDNA clone was found to be larger in the former vectors. The subclone pPR10.1 was used for sequence analysis of the promoter region and the structural gene by the so-called primer walking approach. The partial sequence of the  
25 insert is shown in SEQIDNO: 22. Comparison of the cDNA and the genomic sequence revealed the presence of 4 introns.

#### Example 18

##### Isolation of promoter sequences with high expression levels

30 This example illustrates the feasibility of the "cDNA sequencing method" referred to in the detailed description, in order to obtain transcription promoters from highly expressed genes.

For the isolation and identification of transcription promoter sequences from *Phaffia rhodozyma* genes exhibiting high expression levels, the cDNA library of *Phaffia rhodozyma* was analyzed by the following procedure.

35 The cDNA library was plated on solidified LB-medium containing Amp and 96 colonies were randomly picked for plasmid isolation. The purified plasmid was digested with *Xho*I and *Xba*I and loaded on an agarose gel. The size of the cDNA inserts varied from 0.5 to 3.0 kb. Subsequently, these plasmids were used as template for a single sequence reaction using the T3 primer. For 17 cDNA clones no sequence data were obtained. The sequences obtained were translated in all three reading frames. For

each cDNA sequence the longest deduced amino acid sequences were compared with the SwissProt protein database at EBI using the Blitz program. For 18 deduced amino acid sequences no homology to known proteins was found whereas six amino acid sequences showed significant homology to hypothetical proteins. Fifty-five amino acid sequences were found to have significant homology to proteins for which the function is known. About 50 % (38/79) were found to encode ribosomal proteins of which 12 full-length sequences were obtained.

Table 13. Overview of expressed cDNAs, encoded proteins and reference to the Sequence Listing

cDNA	coding for	SEQIDNO:
10		
10	ubiquitin-40S	24
11	Glu-repr.gene	26
15	18	40S rib.prot S27
35	60S rib.prot P1 $\alpha$	30
38	60S rib.prot L37e	32
46	60S rib.prot L27a	34
64	60S rib.prot L25	36
20	68	60S rib.prot P2
73	40S rib.prot S17A/B	40
76	40S rib.prot S31	42
78	40s rib.prot S10	44
85	60S rib.prot L37A	46
25	87	60S rib.prot L34
95	60S rib.prot S16	50

By sequence homology it was concluded that in *Phaffia* the 40S ribosomal protein S37 is fused to ubiquitin as is found in other organisms as well. The nucleotide sequences and deduced amino acid sequences of the full length cDNA clones are listed in the sequence listing. Six ribosomal proteins were represented in the random pool by more than one individual cDNA clone. The 40S ribosomal proteins S10 (SEQIDNO:44), S37 (+ ubiquitin) (SEQIDNO:24) and S27 (SEQIDNO:28) were represented twice and 60S (acidic) ribosomal proteins P2 (SEQIDNO:38), L37 (SEQIDNO:46) and L25 (SEQIDNO:36) found three times. From these results we conclude, that these proteins are encoded by multiple genes or that these genes are highly expressed. Therefore isolation of these promoter sequences are new and promising target sequences to isolate high level expression signals from *Phaffia rhodozyma*. Furthermore, a cDNA clone was isolated which showed 50 % homology to an abundant glucose-repressible gene from *Neurospora crassa* (Curr. genet. 14: 545-551 (1988)). The nucleotide sequence and the deduced amino acid sequence is shown in SEQIDNO:26. One of the advantages of such a promoter sequence is that it can be used to separated growth (biomass accumulation) and gene expression (product accumulation) in large scale *Phaffia* fermentation.

For the isolation of the promoter sequences of interest (as outlined above) a fragment from the corresponding cDNA clone can be used as probe to screen the genomic library of *Phaffia rhodozyma* following the approach as described for the GAPDH-gene promoter (Example 3, *supra*). Based on the determined nucleotide sequence of the promoter, specific oligonucleotides can be designed to construct a transcription fusion between the promoter and any gene of interest by the fusion PCR technique, following the procedure as outlined in Example 5 (*supra*).

#### Example 19

##### Isolation of carotenogenic genes by heterologous hybridization

For the identification and isolation of corresponding carotenoid biosynthetic pathway genes from organisms related to *Phaffia rhodozyma* heterologous hybridization experiments were carried out under conditions of moderate stringency. In these experiments chromosomal DNA from two carotenogenic fungi (*Neurospora crassa* and *Blakeslea trispora*) and the yeasts *S. cerevisiae* and three yeast and fungal species from the genus *Cystofylobasidium* was used. These three carotenogenic yeasts are, based on phylogenetic studies, the ones most related to *P. rhodozyma*.

Chromosomal DNA from the yeast species *Cystofylobasidium infirmo-miniatum* (CBS 323), *C. bisporidii* (CBS 6346) and *C. capitatum* (CBS 6358) was isolated according the method as developed for *Phaffia rhodozyma*, described in example 3 of European patent application 0 590 707 A1; the relevant portions of which herein incorporated by reference. Isolation of chromosomal DNA from the fungi *Neurospora crassa* and *Blakeslea trispora* was essentially carried as described by Kolar et al. (Gene, 62: 127-134), the relevant parts of which are herein incorporated by reference.

Chromosomal DNA (5 µg) of *C. infirmo-miniatum*, *C. bisporidii*, *C. capitatum*, *S. cerevisiae*, *P. rhodozyma*, *N. crassa* and *B. trispora* was digested using *EcoRI*. The DNA fragments were separated on a 0.8% agarose gel, blotted and hybridized using the following conditions.

Hybridization was carried out at two temperatures (50 °C and 55 °C) using four different <sup>32</sup>P labelled *Phaffia* probes. The probes were made using random primed hexanucleotide labellings reactions using the *XhoI-XbaI* fragment(s) from the cDNA clones pPRcrtE, pPRcrtB, pPRcrtI and pPRidi as template. Hybridization was carried out o/n (16 h) at the indicated temperatures. After hybridization the filters were washed 2 times for 30 min. at the hybridization temperatures using a solution of 3\*SSC; 0.1 % SDS; 0.05% sodiumpyrophosphate. Films were developed after exposure of the filters to X-ray films in a cassette at -80 °C for 20 h.

Using the cDNA clone of *crtE* of *P. rhodozyma* faint signals were obtained for *C. infirmo-miniatum*, *C. capitatum*. Using the cDNA clone of *crtB* of *P. rhodozyma* strong signals were obtained to the high molecular weight portion of DNA from *C. infirmo-miniatum* and *C. capitatum*. Furthermore a strong signal was obtained in the lane loaded with digested chromosomal DNA from *B. trispora*. Only a faint signal was obtained for *C. capitatum* at 50 °C using the cDNA clone of *crtI* of *P. rhodozyma*. Using the cDNA clone of *idi* of *P. rhodozyma* faint signals were obtained with chromosomal DNA from *C. infirmo-miniatum*, *C. bisporidii* and *C. capitatum* at both temperatures. A strong signal was obtained in the lane loaded with digested chromosomal DNA from *B. trispora*.

We conclude, that carotenoid biosynthesis cDNAs or genes, or *idi* cDNAs or genes, can be isolated from other organisms, in particular from other yeast species by cross-hybridisation with the cDNA fragments coding for *P. rhodozyma* carotenoid biosynthesis enzymes, or isopentenyl pyrophosphate isomerase coding sequences respectively, using moderately stringent hybridisation and washing conditions (50 °C to 55 °C, 3xSSC).

#### Deposited microorganisms

*E. coli* containing pGB-Ph9 has been deposited at the Centraal Bureau voor Schimmelcultures, Oosterstraat 1, Baarn, The Netherlands, on June 23, 1993, under accession number CBS 359.3.

The following strains have been deposited under the Budapest Treaty at the Centraal Bureau voor Schimmelcultures, Oosterstraat 1, Baarn, The Netherlands, on February 26, 1996:

ID nr.	Organism	relevant feature	Deposit number
DS31855	<i>E. coli</i>	<i>crtY</i> of <i>P. rhodozyma</i>	CBS 232.96
DS31856	<i>E. coli</i>	<i>crtI</i> of <i>P. rhodozyma</i>	CBS 233.96
DS31857	<i>E. coli</i>	<i>crtE</i> of <i>P. rhodozyma</i>	CBS 234.96
DS31858	<i>E. coli</i>	<i>crtB</i> of <i>P. rhodozyma</i>	CBS 235.96

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

## (i) APPLICANT:

- (A) NAME: Gist-brocades B.V.
- (B) STREET: Wateringseweg 1
- (C) CITY: Delft
- (E) COUNTRY: The Netherlands
- (F) POSTAL CODE (ZIP): 2611 XT

10

- (ii) TITLE OF INVENTION: Improved methods for transforming *Phaffia* and recombinant DNA for use therein

15

- (iii) NUMBER OF SEQUENCES: 51

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

20

## (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER:

25

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

- (ii) MOLECULE TYPE: DNA (genomic)

35

- (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: AB3005

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

45

CGGGATCCAA RCTNACNGGN ATGGC

25

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

- (ii) MOLECULE TYPE: DNA (genomic)

55

- (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: AB3006

60

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: one\_of(12)
- (D) OTHER INFORMATION: /note= "N at position 12 is inosine"

65

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

70



CGGGATCCRT ANCCVYAYTC RTTTCRTAC CA

32

(2) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: AB4206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20 GCGTGACTTC TGGCCAGCCA CGATAGC

27

(2) INFORMATION FOR SEQ ID NO:4:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: AB5126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 TTCAATCCAC ATGATGGTAA GAGTGTAGA GA

32

(2) INFORMATION FOR SEQ ID NO:5:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: AB5127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

60 CTTACCATCA TGTTGATTGA ACAAGATGGA T

31

(2) INFORMATION FOR SEQ ID NO:6:

- 65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 70

(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
5 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: AB5177  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
10 CCCAAGCTTC TCGAGGTACC TGGTGGGTGC ATGTATGTAC

40

(2) INFORMATION FOR SEQ ID NO:7:  
15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
25 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: AB5137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
30 CCCAAGGCCTA AAACGGATCC CTCCTAACCC

30

(2) INFORMATION FOR SEQ ID NO:8:  
35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
45 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: AB5138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
50 GCCAAGCTTC TCGAGCTTGA TCAGATAAAG ATAGAGAT

38

(2) INFORMATION FOR SEQ ID NO:9:  
55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2309 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

65 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Phaffia rhodozyma*  
(B) STRAIN: CBS 6938  
70

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 300..330

5 (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 331..530

10 (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 531..578

(ix) FEATURE:  
 (A) NAME/KEY: intron  
 15 (B) LOCATION: 579..668

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 669..690

20 (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 691..767

25 (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 768..805

(ix) FEATURE:  
 30 (A) NAME/KEY: intron  
 (B) LOCATION: 806..905

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 35 (B) LOCATION: 906..923

(ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 924..1030

40 (ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 1031..1378

45 (ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 1379..1508

(ix) FEATURE:  
 50 (A) NAME/KEY: exon  
 (B) LOCATION: 1509..2020

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 55 (B) LOCATION: join(300..330, 531..578, 669..690, 768..805, 906  
 ..923, 1031..1378, 1509..2020)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

60 GCTATGAGCA AGCACAACTG GGCACCGAAC GAGAACAGTA ACTGTCCGTA TCTTCCACC 60

GACACGAGGC GTCTCCCGGC GGCACCGCC GGTGCCCCC TCCTCTTACG TCAGCCACC 120

65 AGTTTCTTC CATCTCTTC TCTCTCTTC CAAAGTCTT TCAGTTTAA ACGGCCCCA 180

AAAAAGAAG AGGCGACTT TCTTTCTT CTCCCATCA TCCACAAAGA TCTCTCTCT 240

TCAACAACAA CTACTACTAC TACCACTACC ACCACTACTT CTCTAACA CTTAACATC 299

70

	ATG GCT GTC AAG GTT GGA ATC AAC GGT TTC G GTAATGTGTTT GTTTTCTCT	350
	Met Ala Val Lys Val Gly Ile Asn Gly Phe	
	1 5 10	
5	TGAGCTCCCC CATCGGTCTT TTCGCTGTGTC CATGTTCTTT TTTCCTTTCC TTTCCTTTTC	410
	TTTTTCTCC CCAGTGCCTT TTTTCTTCTT ATTCTTTTTT TTTCCTTTTC CTCTGGCCTT	470
	CATGCATGCG ACTAACACCA TCTCATCTCA TCTCACTCTG CCTGCTCTTA CCTCCTACAG	530
10	GA CGA ATC GGA CGA ATC GTC CTT CGA AAC GCT ATC ATC CAC GGT GAT A	578
	Gly Arg Ile Gly Arg Ile Val Leu Arg Asn Ala Ile Ile His Gly Asp	
	15 20 25	
15	GTCAGTATTT TTTTAATTTC TTTTCTTCCC CATCAATTTC CCTCTGCTCC TTACTCATC	638
	TCTTTCCATC TCTCTCCAC TCTCCTACAG TC GAT GTC GTC GCC ATC AAC GA	690
	Ile Asp Val Val Ala Ile Asn Asp	
	30	
20	GTGCGTCTAG ATCGACCATC TGTGCTGCG CCCAAACACC GTCTGACACC ATCCTGTAA	750
	CTTTCTCTC CTCCAAG C CCT TTC ATC GAT CIT GAG TAC ATG GTC TAC ATG	801
	Pro Phe Ile Asp Leu Glu Tyr Met Val Tyr Met	
25	35 40 45	
	TTC A GTAAGTCTCC CTCCCTCTCA AAAAGCCGAA ACAAGCCGA ACAGAACCCG	855
	Phe	
30	ATCTAACCAT TCGTCTCTCT TCCCTTTCCT CTTCGGTCTC TCCCTCACAG AG TAC	910
	Lys Tyr	
35	GAC TCC ACC CAC G GTTCGTCCAT CCCCTCTCTT GTCCCGAACA TCTCCGACCG	963
	Asp Ser Thr His	
	50	
	GGCCTTTTC ATCTCCGAT CCGTTCGGT ACTAACCCAT ACCGTACCT TCGTCCATC	1023
40	CCCTCAG GT GTC TTC AAG GGA TCC GTC GAG ATC AAG GAC GGC AAG CTC	1071
	Gly Val Phe Lys Gly Ser Val Glu Ile Lys Asp Gly Lys Leu	
	55 60 65	
45	GTG ATC GAG GGC AAG CCC ATC GTC GTC TAC GGT GAG CGA GAC CCC GCC	1119
	Val Ile Glu Gly Lys Pro Ile Val Val Tyr Gly Glu Arg Asp Pro Ala	
	70 75 80	
	AAC ATC CAG TGG GGA GCT GCC GGT GCC GAC TAC GTC GTC GAG TCC ACC	1167
50	Asn Ile Gln Trp Gly Ala Ala Gly Ala Asp Tyr Val Val Glu Ser Thr	
	85 90 95	
	GGT GTC TTC ACC ACC CAG GAG AAG GCC GAG CTC CAC CTC AAG GGA GGA	1215
	Gly Val Phe Thr Thr Gln Glu Lys Ala Glu Leu His Leu Lys Gly Gly	
55	100 105 110	
	GCC AAG AAG GTC GTC ATC TCT GCC OCT TCG GCC GAT GCC CCC ATG TTC	1263
	Ala Lys Lys Val Val Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe	
	115 120 125 130	
60	GTC TGC GGT GTT AAC CTC GAC AAG TAC GAC CCC AAG TAC ACC GTC GTC	1311
	Val Cys Gly Val Asn Leu Asp Lys Tyr Asp Pro Lys Tyr Thr Val Val	
	135 140 145	
65	TCC AAC GCT TCG TGC ACC ACC AAC TGC TTG GCT CCC CTC GGC AAG GTC	1359
	Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Gly Lys Val	
	150 155 160	
70	ATC CAC GAC AAC TAC ACC A GTCACTCCTT TNCPTTGGAC TTGTCTGGCC	1408

	Ile His Asp Asn Tyr Thr	
	165	
	TTTTCTTTGT TGGTCTTTT CCTTTTGTC AACCATCCAT ACTCACCCTG TTTTTCACCT	1468
5	TCTTTTCTTT CATTCACGTA TCCCCCTCC GGTCCACCAG TT GTC GAG GGT CTC	1522
	Ile Val Glu Gly Leu	
	170	
10	ATG ACC ACC GTC CAC GCC ACC ACC GCC ACC CAG AAG ACC GTC GAC GGT	1570
	Met Thr Thr Val His Ala Thr Thr Ala Thr Gln Lys Thr Val Asp Gly	
	175 180 185	
	CCT TCC AAC AAG GAC TGG CGA GGA GGT CGA GGA GCT GGT GCC AAC ATC	1618
15	Pro Ser Asn Lys Asp Trp Arg Gly Gly Arg Gly Ala Gly Ala Asn Ile	
	190 195 200 205	
	ATT CCC TCC TCC ACC GGA GCC GCC AAG GCC GTC GGT AAG GTT ATC CCC	1666
20	Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro	
	210 215 220	
	TCC CTC AAC GGA AAG CTC ACC GGA ATG GCC TTC CGA GTG CCC ACC CCC	1714
	Ser Leu Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro	
	225 230 235	
25	GAT GTC TCC GTC GTC GAT CTT GTC GTC CGA ATC GAG AAG GGC GCC TCT	1762
	Asp Val Ser Val Val Asp Leu Val Val Arg Ile Glu Lys Gly Ala Ser	
	240 245 250	
30	TAC GAG GAG ATC AAG GAG ACC ATC AAG AAG GCC TCC CAG ACC CCT GAG	1810
	Tyr Glu Glu Ile Lys Glu Thr Ile Lys Lys Ala Ser Gln Thr Pro Glu	
	255 260 265	
	CTC AAG GGT ATC CTG AAC TAC ACC GAC GAC CAG GTC GTC TCC ACC GAT	1858
35	Leu Lys Gly Ile Leu Asn Tyr Thr Asp Asp Gln Val Val Ser Thr Asp	
	270 275 280 285	
	TTC ACC GGT GAC TCT GCC TCC TCC ACC TTC GAC GCC CAG GGC GGT ATC	1906
40	Phe Thr Gly Asp Ser Ala Ser Ser Thr Phe Asp Ala Gln Gly Gly Ile	
	290 295 300	
	TCC CTT AAC GGA AAC TTC GTC AAG CTT GTC TCC TGG TAC GAC AAC GAG	1954
	Ser Leu Asn Gly Asn Phe Val Lys Leu Val Ser Trp Tyr Asp Asn Glu	
	305 310 315	
45	TGG GGA TAC TCT GCC CGA GTC TGC GAC CTT GTT TCT TAC ATC GCC GCC	2002
	Trp Gly Tyr Ser Ala Arg Val Cys Asp Leu Val Ser Tyr Ile Ala Ala	
	320 325 330	
50	CAG GAC GCC AAG GCC TAAACGGTTC TCTCCAAACC CTCTCCCCCTT TTGCCCTGCC	2057
	Gln Asp Ala Lys Ala	
	335	
	CATTGAATTG ATTCCCTAAA TAGAATATCC CACTTTCTTT TATGCTCTAC CTATGATCAG	2117
55	TTTATCTGTC TTTTCTTTTG TGCGTGTCGG TTGTGGGACT GTACCCACCT CTTGAGGGAC	2177
	AAGGCAAGAA GTGAGCAAGA TATGAACAAG AACAACAAG AAAAAGAGAC AAAGAAAAAA	2237
60	AAAAGGAAAG AGAAAACAAT CCCCCCCCCC CCCCACAAAA AAATCTCTAT CTTTATCTGA	2297
	TCAAGAGATT AT	2309
65	(2) INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 338 amino acids	
	(B) TYPE: amino acid	
70	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5 Met Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile  
    1                  5                  10                  15  
 Val Leu Arg Asn Ala Ile Ile His Gly Asp Ile Asp Val Val Ala Ile  
           20                  25                  30  
 10 Asn Asp Pro Phe Ile Asp Leu Glu Tyr Met Val Tyr Met Phe Lys Tyr  
           35                  40                  45  
 15 Asp Ser Thr His Gly Val Phe Lys Gly Ser Val Glu Ile Lys Asp Gly  
           50                  55                  60  
 Lys Leu Val Ile Glu Gly Lys Pro Ile Val Val Tyr Gly Glu Arg Asp  
           65                  70                  75                  80  
 20 Pro Ala Asn Ile Gln Trp Gly Ala Ala Gly Ala Asp Tyr Val Val Glu  
                   85                  90                  95  
 Ser Thr Gly Val Phe Thr Thr Gln Glu Lys Ala Glu Leu His Leu Lys  
 25          100                  105                  110  
 Gly Gly Ala Lys Lys Val Val Ile Ser Ala Pro Ser Ala Asp Ala Pro  
           115                  120                  125  
 30 Met Phe Val Cys Gly Val Asn Leu Asp Lys Tyr Asp Pro Lys Tyr Thr  
           130                  135                  140  
 Val Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Gly  
           145                  150                  155                  160  
 35 Lys Val Ile His Asp Asn Tyr Thr Ile Val Glu Gly Leu Met Thr Thr  
                   165                  170                  175  
 Val His Ala Thr Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Asn  
 40          180                  185                  190  
 Lys Asp Trp Arg Gly Gly Arg Gly Ala Gly Ala Asn Ile Ile Pro Ser  
           195                  200                  205  
 45 Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Ser Leu Asn  
           210                  215                  220  
 Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asp Val Ser  
           225                  230                  235                  240  
 50 Val Val Asp Leu Val Val Arg Ile Glu Lys Gly Ala Ser Tyr Glu Glu  
           245                  250                  255  
 Ile Lys Glu Thr Ile Lys Lys Ala Ser Gln Thr Pro Glu Leu Lys Gly  
 55          260                  265                  270  
 Ile Leu Asn Tyr Thr Asp Asp Gln Val Val Ser Thr Asp Phe Thr Gly  
           275                  280                  285  
 60 Asp Ser Ala Ser Ser Thr Phe Asp Ala Gln Gly Gly Ile Ser Leu Asn  
           290                  295                  300  
 Gly Asn Phe Val Lys Leu Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr  
 65          305                  310                  315                  320  
 Ser Ala Arg Val Cys Asp Leu Val Ser Tyr Ile Ala Ala Gln Asp Ala  
           325                  330                  335  
 70 Lys Ala

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:1..385

## (ix) FEATURE:

- (A) NAME/KEY: TATA signal
- (B) LOCATION:249..263
- (D) OTHER INFORMATION:/label= putative

## (ix) FEATURE:

- (A) NAME/KEY: misc signal
- (B) LOCATION:287..302
- (D) OTHER INFORMATION:/function= "cap-signal"  
/label= putative

## (ix) FEATURE:

- (A) NAME/KEY: misc RNA
- (B) LOCATION:386..388
- (D) OTHER INFORMATION:/function= "start of CDS"

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION:85
- (D) OTHER INFORMATION:/note= "uncertain"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

45  TGGTGGGTGC ATGTATGTAC GTGAGTGAGT GGGGGGGAAA GGCGAGTACG TGTGTGTACG      60
    CGCAAGGAAG AACAAAGAAG CGCANGCTAT GAGCAAGCAC AACTGGGCAC CGAACGAGAA      120
50  CAGTAAC1GT CGGTATCTTC CCACGACAC GAGGCGTTC CCGGGGCAA CCGCCGGTGC      180
    CCCCCTCCGC TTACGTCAGC CACCCAGTTT TCTTCGATCT CTTTCTCTCT CCTTCCAAAA      240
    GTCTTTCAGT TTTAAACGGC CCCCACAAAA AGAAGAGGCG ACTTTTCTCT TCCTTCTCTC      300
55  CCATCATCCA CAAAGATCTC TCTTCTTCAA CAACAAC1AC TACTACTACC ACTACCACCA      360
    CTACTCTCTT AACACTCTTA CCATCATG      388

```

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phaffia rhodozyma*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 225..2246

(D) OTHER INFORMATION: /product= "PRcrTB"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15	TCTAGAACTA GTGGATCCCC CGGCTGCAG GAATTGGCA CGAGCGGAAA CAAGAAGTGG	60
	ACACAGAGAG ATCTTTGCTG AAGAGTTGTA TTCCAGAAAG GGAAAACAAA GGAAAGAAGC	120
20	GGCGAAGCAC ATCAACCACT TCAGCAAGCC GGTCCAGCCC GATCTCGGAT AGACATCATC	180
	TTACCCCACT CGTATCATCC CCAACAGATA GAGTTTITGT CGCA ATG ACG GCT CTC	236
	Met Thr Ala Leu	
	1	
25	GCA TAT TAC CAG ATC CAT CTG ATC TAT ACT CTC CCA ATT CTT GGT CTT	284
	Ala Tyr Tyr Gln Ile His Leu Ile Tyr Thr Leu Pro Ile Leu Gly Leu	
	5 10 15 20	
30	CTC GGC CTG CTC ACT TCC CCG ATT TTG ACA AAA TTT GAC ATC TAC AAA	332
	Leu Gly Leu Leu Thr Ser Pro Ile Leu Thr Lys Phe Asp Ile Tyr Lys	
	25 30 35	
35	ATA TGG ATC CTC GTA TTT ATT GCG TTT AGT GCA ACC ACA CCA TGG GAC	380
	Ile Ser Ile Leu Val Phe Ile Ala Phe Ser Ala Thr Thr Pro Trp Asp	
	40 45 50	
	TCA TGG ATC ATC AGA AAT GGC GCA TGG ACA TAT CCA TCA GCG GAG AGT	428
	Ser Trp Ile Ile Arg Asn Gly Ala Trp Thr Tyr Pro Ser Ala Glu Ser	
	55 60 65	
40	GGC CAA GGC GTG TTT GGA ACG TTT CTA GAT GTT CCA TAT GAA GAG TAC	476
	Gly Gln Gly Val Phe Gly Thr Phe Leu Asp Val Pro Tyr Glu Glu Tyr	
	70 75 80	
45	GCT TTC TTT GTC ATT CAA ACC GTA ATC ACC GGC TTG GTC TAC GTC TTG	524
	Ala Phe Phe Val Ile Gln Thr Val Ile Thr Gly Leu Val Tyr Val Leu	
	85 90 95 100	
50	GCA ACT AGG CAC CTT CTC CCA TCT CTC GCG CTT CCC AAG ACT AGA TGG	572
	Ala Thr Arg His Leu Leu Pro Ser Leu Ala Leu Pro Lys Thr Arg Ser	
	105 110 115	
55	TCC GCC CTT TCT CTC GCG CTC AAG GCG CTC ATC CCT CTG CCC ATT ATC	620
	Ser Ala Leu Ser Leu Ala Leu Lys Ala Leu Ile Pro Leu Pro Ile Ile	
	120 125 130	
60	TAC CTA TTT ACC GCT CAC CCC AGC CCA TGG CCC GAC CCG CTC GTG ACA	668
	Tyr Leu Phe Thr Ala His Pro Ser Pro Ser Pro Asp Pro Leu Val Thr	
	135 140 145	
	GAT CAC TAC TTC TAC ATG CGG GCA CTC TCC TTA CTC ATC ACC CCA CCT	716
	Asp His Tyr Phe Tyr Met Arg Ala Leu Ser Leu Ile Thr Pro Pro	
	150 155 160	
65	ACC ATG CTC TTG GCA GCA TTA TCA GGC GAA TAT GCT TTC GAT TGG AAA	764
	Thr Met Leu Leu Ala Ala Leu Ser Gly Glu Tyr Ala Phe Asp Trp Lys	
	165 170 175 180	
70	AGT GGC CGA GCA AAG TCA ACT ATT GCA GCA ATC ATG ATC CCG ACG GTG	812
	Ser Gly Arg Ala Lys Ser Thr Ile Ala Ala Ile Met Ile Pro Thr Val	



	185	190	195	
5	TAT CTG ATT TGG GTA GAT TAT GTT GCT GTC GGT CAA GAC TCT TGG TCG Tyr Leu Ile Trp Val Asp Tyr Val Ala Val Gly Gln Asp Ser Trp Ser 200 205 210			860
10	ATC AAC GAT GAG AAG ATT GTA GGG TGG AGG CTT GGA GGT GTA CTA CCC Ile Asn Asp Glu Lys Ile Val Gly Trp Arg Leu Gly Gly Val Leu Pro 215 220 225			908
15	ATT GAG GAA GCT ATG TTC TTC TTA CTG ACG AAT CTA ATG ATT GTT CTG Ile Glu Glu Ala Met Phe Phe Leu Leu Thr Asn Leu Met Ile Val Leu 230 235 240			956
20	GGT CTG TCT GCC TGC GAT CAT ACT CAG GCC CTA TAC CTG CTA CAC GGT Gly Leu Ser Ala Cys Asp His Thr Gln Ala Leu Tyr Leu Leu His Gly 245 250 255 260			1004
25	CGA ACT ATT TAT GGC AAC AAA AAG ATG CCA TCT TCA TTT CCC CTC ATT Arg Thr Ile Tyr Gly Asn Lys Lys Met Pro Ser Ser Phe Pro Leu Ile 265 270 275			1052
30	ACA CCG OCT GTG CTC TCC CTG TTT TTT AGC AGC CGA CCA TAC TCT TCT Thr Pro Pro Val Leu Ser Leu Phe Phe Ser Ser Arg Pro Tyr Ser Ser 280 285 290			1100
35	CAG CCA AAA CGT GAC TTG GAA CTG GCA GTC AAG TTG TTG GAG AAA AAG Gln Pro Lys Arg Asp Leu Glu Leu Ala Val Lys Leu Leu Glu Lys Lys 295 300 305			1148
40	AGC CGG AGC TTT TTT GTT GCC TCG GCT GGA TTT CCT AGC GAA GTT AGG Ser Arg Ser Phe Phe Val Ala Ser Ala Gly Phe Pro Ser Glu Val Arg 310 315 320			1196
45	GAG AGG CTG GTT GGA CTA TAC GCA TTC TGC CGG GTG ACT GAT GAT CTT Glu Arg Leu Val Gly Leu Tyr Ala Phe Cys Arg Val Thr Asp Asp Leu 325 330 335 340			1244
50	ATC GAC TCT CCT GAA GTA TCT TCC AAC CCG CAT GCC ACA ATT GAC ATG Ile Asp Ser Pro Glu Val Ser Ser Asn Pro His Ala Thr Ile Asp Met 345 350 355			1292
55	GTC TCC GAT TTT CTT ACC CTA CTA TTT GGG CCC CCG CTA CAC CCT TCG Val Ser Asp Phe Leu Thr Leu Leu Phe Gly Pro Pro Leu His Pro Ser 360 365 370			1340
60	CAA OCT GAC AAG ATC CTT TCT TCG CCT TTA CTT CCT CCT TCG CAC CCT Gln Pro Asp Lys Ile Leu Ser Ser Pro Leu Leu Pro Pro Ser His Pro 375 380 385			1388
65	TCC CGA CCC ACG GGA ATG TAT CCC CTC CCG CCT CCT CCT TCG CTC TCG Ser Arg Pro Thr Gly Met Tyr Pro Leu Pro Pro Pro Pro Ser Leu Ser 390 395 400			1436
70	CCT GCC GAG CTC GTT CAA TTC CTT ACC GAA AGG GTT CCC GTT CAA TAC Pro Ala Glu Leu Val Gln Phe Leu Thr Glu Arg Val Pro Val Gln Tyr 405 410 415 420			1484
75	CAT TTC GCC TTC AGG TTG CTC GCT AAG TTG CAA GGG CTG ATC CCT CGA His Phe Ala Phe Arg Leu Leu Ala Lys Leu Gln Gly Leu Ile Pro Arg 425 430 435			1532
80	TAC CCA CTC GAC GAA CTC CTT AGA GGA TAC ACC ACT GAT CTT ATC TTT Tyr Pro Leu Asp Glu Leu Leu Arg Gly Tyr Thr Thr Asp Leu Ile Phe 440 445 450			1580
85	CCC TTA TCG ACA GAG GCA GTC CAG GCT CGG AAG ACG CCT ATC GAG ACC Pro Leu Ser Thr Glu Ala Val Gln Ala Arg Lys Thr Pro Ile Glu Thr 455 460 465			1628

	ACA GCT GAC TTG CTG GAC TAT GGT CTA TGT GTA GCA GGC TCA GTC GCC Thr Ala Asp Leu Leu Asp Tyr Gly Leu Cys Val Ala Gly Ser Val Ala 470 475 480	1676
5	GAG CTA TTG GTC TAT GTC TCT TGG GCA AGT GCA CCA AGT CAG GTC CCT Glu Leu Leu Val Tyr Val Ser Trp Ala Ser Ala Pro Ser Gln Val Pro 485 490 495 500	1724
10	GCC ACC ATA GAA GAA AGA GAA GCT GTG TTA GTG GCA AGC CGA GAG ATG Ala Thr Ile Glu Glu Arg Glu Ala Val Leu Val Ala Ser Arg Glu Met 505 510 515	1772
15	GGA ACT GCC CTT CAG TTG GTG AAC ATT GCT AGG GAC ATT AAA GGG GAC Gly Thr Ala Leu Gln Leu Val Asn Ile Ala Arg Asp Ile Lys Gly Asp 520 525 530	1820
20	GCA ACA GAA GGG AGA TTT TAC CTA CCA CTC TCA TTC TTT GGT CTT CGG Ala Thr Glu Gly Arg Phe Tyr Leu Pro Leu Ser Phe Phe Gly Leu Arg 535 540 545	1868
25	GAT GAA TCA AAG CTT GCG ATC CCG ACT GAT TGG ACG GAA CCT CGG CCT Asp Glu Ser Lys Leu Ala Ile Pro Thr Asp Trp Thr Glu Pro Arg Pro 550 555 560	1916
30	CAA GAT TTC GAC AAA CTC CTC AGT CTA TCT CCT TCG TCC ACA TTA CCA Gln Asp Phe Asp Lys Leu Leu Ser Leu Ser Pro Ser Ser Thr Leu Pro 565 570 575 580	1964
35	TCT TCA AAC GCC TCA GAA AGC TTC CGG TTC GAA TGG AAG ACG TAC TCG Ser Ser Asn Ala Ser Glu Ser Phe Arg Phe Glu Trp Lys Thr Tyr Ser 585 590 595	2012
40	CTT CCA TTA GTC GCC TAC GCA GAG GAT CTT GCC AAA CAT TCT TAT AAG Leu Pro Leu Val Ala Tyr Ala Glu Asp Leu Ala Lys His Ser Tyr Lys 600 605 610	2060
45	GGA ATT GAC CGA CTT CCT ACC GAG GTT CAA GCG GGA ATG CGA GCG GCT Gly Ile Asp Arg Leu Pro Thr Glu Val Gln Ala Gly Met Arg Ala Ala 615 620 625	2108
50	TGC GCG AGC TAC CTA CTG ATC GGC CGA GAG ATC AAA GTC GTT TGG AAA Cys Ala Ser Tyr Leu Leu Ile Gly Arg Glu Ile Lys Val Val Trp Lys 630 635 640	2156
55	GGA GAC GTC GGA GAG AGA AGG ACA GTT GCC GGA TGG AGG AGA GTA CCG Gly Asp Val Gly Glu Arg Arg Thr Val Ala Gly Trp Arg Arg Val Arg 645 650 655 660	2204
60	AAA GTC TTG AGT GTG GTC ATG AGC GGA TGG GAA GGG CAG TAAGACAGCG Lys Val Leu Ser Val Val Met Ser Gly Trp Glu Gly Gln 665 670	2253
65	GAAGAATACC GACAGACAAT GATGAGTGAG AATAAAATCA TCTCAATCT TCTTTCTCTA GGTGCTCTTT TTGTGTTTCT ATTATGACCA ACTCTAAAGG AACTGGCCTT GCAGATATTT CCTTCCCCC CATCTTCTC CTTCATCG TTGTCTCTT CCATTTTGT GGGTTTACTA TGTCATTTCT TTTTCTTGCT TTTTCTTATC AATCTAGACA ATTCTATAGA TGTTTAGAAT TTATACATTG ACAGGTTATA GACCATAAAG ACTAAAAAAA AAAAAAAAAA AAA	2313 2373 2433 2493 2546

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 673 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5 Met Thr Ala Leu Ala Tyr Tyr Gln Ile His Leu Ile Tyr Thr Leu Pro  
 1 5 10 15  
 Ile Leu Gly Leu Leu Gly Leu Leu Thr Ser Pro Ile Leu Thr Lys Phe  
 20 25 30  
 10 Asp Ile Tyr Lys Ile Ser Ile Leu Val Phe Ile Ala Phe Ser Ala Thr  
 35 40 45  
 Thr Pro Trp Asp Ser Trp Ile Ile Arg Asn Gly Ala Trp Thr Tyr Pro  
 15 50 55 60  
 Ser Ala Glu Ser Gly Gln Gly Val Phe Gly Thr Phe Leu Asp Val Pro  
 65 70 75 80  
 20 Tyr Glu Glu Tyr Ala Phe Phe Val Ile Gln Thr Val Ile Thr Gly Leu  
 85 90 95  
 Val Tyr Val Leu Ala Thr Arg His Leu Leu Pro Ser Leu Ala Leu Pro  
 100 105 110  
 25 Lys Thr Arg Ser Ser Ala Leu Ser Leu Ala Leu Lys Ala Leu Ile Pro  
 115 120 125  
 Leu Pro Ile Ile Tyr Leu Phe Thr Ala His Pro Ser Pro Ser Pro Asp  
 130 135 140  
 Pro Leu Val Thr Asp His Tyr Phe Tyr Met Arg Ala Leu Ser Leu Leu  
 145 150 155 160  
 35 Ile Thr Pro Pro Thr Met Leu Leu Ala Ala Leu Ser Gly Glu Tyr Ala  
 165 170 175  
 Phe Asp Trp Lys Ser Gly Arg Ala Lys Ser Thr Ile Ala Ala Ile Met  
 180 185 190  
 40 Ile Pro Thr Val Tyr Leu Ile Trp Val Asp Tyr Val Ala Val Gly Gln  
 195 200 205  
 Asp Ser Trp Ser Ile Asn Asp Glu Lys Ile Val Gly Trp Arg Leu Gly  
 210 215 220  
 Gly Val Leu Pro Ile Glu Glu Ala Met Phe Phe Leu Leu Thr Asn Leu  
 225 230 235 240  
 50 Met Ile Val Leu Gly Leu Ser Ala Cys Asp His Thr Gln Ala Leu Tyr  
 245 250 255  
 Leu Leu His Gly Arg Thr Ile Tyr Gly Asn Lys Lys Met Pro Ser Ser  
 260 265 270  
 55 Phe Pro Leu Ile Thr Pro Pro Val Leu Ser Leu Phe Phe Ser Ser Arg  
 275 280 285  
 Pro Tyr Ser Ser Gln Pro Lys Arg Asp Leu Glu Leu Ala Val Lys Leu  
 290 295 300  
 60 Leu Glu Lys Lys Ser Arg Ser Phe Phe Val Ala Ser Ala Gly Phe Pro  
 305 310 315 320  
 65 Ser Glu Val Arg Glu Arg Leu Val Gly Leu Tyr Ala Phe Cys Arg Val  
 325 330 335  
 Thr Asp Asp Leu Ile Asp Ser Pro Glu Val Ser Ser Asn Pro His Ala  
 340 345 350  
 70

Thr Ile Asp Met Val Ser Asp Phe Leu Thr Leu Leu Phe Gly Pro Pro  
 355 360 365  
 Leu His Pro Ser Gln Pro Asp Lys Ile Leu Ser Ser Pro Leu Leu Pro  
 5 370 375 380  
 Pro Ser His Pro Ser Arg Pro Thr Gly Met Tyr Pro Leu Pro Pro Pro  
 385 390 395 400  
 10 Pro Ser Leu Ser Pro Ala Glu Leu Val Gln Phe Leu Thr Glu Arg Val  
 405 410 415  
 Pro Val Gln Tyr His Phe Ala Phe Arg Leu Leu Ala Lys Leu Gln Gly  
 420 425 430  
 15 Leu Ile Pro Arg Tyr Pro Leu Asp Glu Leu Leu Arg Gly Tyr Thr Thr  
 435 440 445  
 Asp Leu Ile Phe Pro Leu Ser Thr Glu Ala Val Gln Ala Arg Lys Thr  
 20 450 455 460  
 Pro Ile Glu Thr Thr Ala Asp Leu Leu Asp Tyr Gly Leu Cys Val Ala  
 465 470 475 480  
 25 Gly Ser Val Ala Glu Leu Leu Val Tyr Val Ser Trp Ala Ser Ala Pro  
 485 490 495  
 Ser Gln Val Pro Ala Thr Ile Glu Glu Arg Glu Ala Val Leu Val Ala  
 500 505 510  
 30 Ser Arg Glu Met Gly Thr Ala Leu Gln Leu Val Asn Ile Ala Arg Asp  
 515 520 525  
 Ile Lys Gly Asp Ala Thr Glu Gly Arg Phe Tyr Leu Pro Leu Ser Phe  
 35 530 535 540  
 Phe Gly Leu Arg Asp Glu Ser Lys Leu Ala Ile Pro Thr Asp Trp Thr  
 545 550 555 560  
 40 Glu Pro Arg Pro Gln Asp Phe Asp Lys Leu Leu Ser Leu Ser Pro Ser  
 565 570 575  
 Ser Thr Leu Pro Ser Ser Asn Ala Ser Glu Ser Phe Arg Phe Glu Trp  
 580 585 590  
 45 Lys Thr Tyr Ser Leu Pro Leu Val Ala Tyr Ala Glu Asp Leu Ala Lys  
 595 600 605  
 His Ser Tyr Lys Gly Ile Asp Arg Leu Pro Thr Glu Val Gln Ala Gly  
 50 610 615 620  
 Met Arg Ala Ala Cys Ala Ser Tyr Leu Leu Ile Gly Arg Glu Ile Lys  
 625 630 635 640  
 55 Val Val Trp Lys Gly Asp Val Gly Glu Arg Arg Thr Val Ala Gly Trp  
 645 650 655  
 Arg Arg Val Arg Lys Val Leu Ser Val Val Met Ser Gly Trp Glu Gly  
 660 665 670  
 60 Gln

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phaffia rhodozyma*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 82..1212

(D) OTHER INFORMATION: /product= "PRcrTE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCAGGAGCC AATTAAAGT GCACTCAGCC ATAGCTAACA CACAGAACTA CACATACATA	60
CACTCATCG GAACACATAG G ATG GAT TAC GCG AAC ATC CTC ACA GCA ATT	111
Met Asp Tyr Ala Asn Ile Leu Thr Ala Ile	
1 5 10	
CCA CTC GAG TTT ACT CCT CAG GAT GAT ATC GTG CTC CTT GAA CCG TAT	159
Pro Leu Glu Phe Thr Pro Gln Asp Asp Ile Val Leu Leu Glu Pro Tyr	
15 20 25	
CAC TAC CTA GGA AAG AAC CCT GGA AAA GAA ATT CGA TCA CAA CTC ATC	207
His Tyr Leu Gly Lys Asn Pro Gly Lys Glu Ile Arg Ser Gln Leu Ile	
30 35 40	
GAG GCT TTC AAC TAT TGG TTG GAT GTC AAG AAG GAG GAT CTC GAG GTC	255
Glu Ala Phe Asn Tyr Trp Leu Asp Val Lys Lys Glu Asp Leu Glu Val	
45 50 55	
ATC CAG AAC GTT GTT GGC ATG CTA CAT ACC GCT AGC TTA TTA ATG GAC	303
Ile Gln Asn Val Val Gly Met Leu His Thr Ala Ser Leu Leu Met Asp	
60 65 70	
GAT GTG GAG GAT TCA TCG GTC CTC AGG CGT GGG TCG OCT GTG GCC CAT	351
Asp Val Glu Asp Ser Ser Val Leu Arg Arg Gly Ser Pro Val Ala His	
75 80 85 90	
CTA ATT TAC GGG ATT CCG CAG ACA ATA AAC ACT GCA AAC TAC GTC TAC	399
Leu Ile Tyr Gly Ile Pro Gln Thr Ile Asn Thr Ala Asn Tyr Val Tyr	
95 100 105	
TTT CTG GCT TAT CAA GAG ATC TTC AAG CTT CGC CCA ACA CCG ATA CCC	447
Phe Leu Ala Tyr Gln Glu Ile Phe Lys Leu Arg Pro Thr Pro Ile Pro	
110 115 120	
ATG OCT GTA ATT OCT OCT TCA TCT GCT TCG CTT CAA TCA TCC GTC TCC	495
Met Pro Val Ile Pro Pro Ser Ser Ala Ser Leu Gln Ser Ser Val Ser	
125 130 135	
TCT GCA TCC TCC TCC TCC TCG GCC TCG TCT GAA AAC GGG GGC ACG TCA	543
Ser Ala Ser Ser Ser Ser Ser Ala Ser Ser Glu Asn Gly Gly Thr Ser	
140 145 150	
ACT CCT AAT TCG CAG ATT CCG TTC TCG AAA GAT ACG TAT CTT GAT AAA	591
Thr Pro Asn Ser Gln Ile Pro Phe Ser Lys Asp Thr Tyr Leu Asp Lys	
155 160 165 170	
GTG ATC ACA GAC GAG ATG CTT TCC CTC CAT AGA GGG CAA GGC CTG GAG	639
Val Ile Thr Asp Glu Met Leu Ser Leu His Arg Gly Gln Gly Leu Glu	
175 180 185	
CTA TTC TGG AGA GAT AGT CTG ACG TGT CCT AGC GAA GAG GAA TAT GTG	687
Leu Phe Trp Arg Asp Ser Leu Thr Cys Pro Ser Glu Glu Tyr Val	
190 195 200	

	AAA ATG GTT CTT GGA AAG ACG GGA GGT TTG TTC CGT ATA GCG GTC AGA Lys Met Val Leu Gly Lys Thr Gly Gly Leu Phe Arg Ile Ala Val Arg 205 210 215	735
5	TTG ATG ATG GCA AAG TCA GAA TGT GAC ATA GAC TTT GTC CAG CTT GTC Leu Met Met Ala Lys Ser Glu Cys Asp Ile Asp Phe Val Gln Leu Val 220 225 230	783
10	AAC TTG ATC TCA ATA TAC TTC CAG ATC AGG GAT GAC TAT ATG AAC CTT Asn Leu Ile Ser Ile Tyr Phe Gln Ile Arg Asp Asp Tyr Met Asn Leu 235 240 245 250	831
15	CAG TCT TCT GAG TAT GCC CAT AAT AAG AAT TTT GCA GAG GAC CTC ACA Gln Ser Ser Glu Tyr Ala His Asn Lys Asn Phe Ala Glu Asp Leu Thr 255 260 265	879
	GAA GGG AAA TTC AGT TTT CCC ACT ATC CAC TCG ATT CAT GCC AAC CCC Glu Gly Lys Phe Ser Phe Pro Thr Ile His Ser Ile His Ala Asn Pro 270 275 280	927
20	TCA TCG AGA CTC GTC ATC AAT ACG TTG CAG AAG AAA TCG ACC TCT CCT Ser Ser Arg Leu Val Ile Asn Thr Leu Gln Lys Lys Ser Thr Ser Pro 285 290 295	975
25	GAG ATC CTT CAC CAC TGT GTA AAC TAC ATG CGC ACA GAA ACC CAC TCA Glu Ile Leu His His Cys Val Asn Tyr Met Arg Thr Glu Thr His Ser 300 305 310	1023
30	TTC GAA TAT ACT CAG GAA GTC CTC AAC ACC TTG TCA GGT GCA CTC GAG Phe Glu Tyr Thr Gln Glu Val Leu Asn Thr Leu Ser Gly Ala Leu Glu 315 320 325 330	1071
35	AGA GAA CTA GGA AGG CTT CAA GGA GAG TTC GCA GAA GCT AAC TCA AGG Arg Glu Leu Gly Arg Leu Gln Gly Glu Phe Ala Glu Ala Asn Ser Arg 335 340 345	1119
40	ATG GAT CTT GGA GAC GTA GAT TCG GAA GGA AGA ACG GGG AAG AAC GTC Met Asp Leu Gly Asp Val Asp Ser Glu Gly Arg Thr Gly Lys Asn Val 350 355 360	1167
45	AAA TTG GAA GCG ATC CTG AAA AAG CTA GCC GAT ATC OCT CTG TGAAAGAACA Lys Leu Glu Ala Ile Leu Lys Lys Leu Ala Asp Ile Pro Leu 365 370 375	1219
	TATTCTCTCT CTGCTCTGTC CGTTCTATC AGGGTTTAT AAGTTGCTC TTTATTCTTA	1279
	AGGGTTTGTC AGATGATTGG ACTTGATGTC CTCATATGCC CGTTCATCTT TTTCACTTCG	1339
50	ACTTTTTTCT CTACCGTGCA TGCCCATTCG CATCTCTTTC TTCATCTTGT GTTTAATTTC	1399
	TTGACATAA CATTAATCAT CGTGCTTCT TCTTTTGGAA GAAATCTCGT GACTTGTTGA	1459
	ACTTCAACTA TAATTAATCA TATCATATC TCAAAGTCTT CGTCTCTCTG CAATGIGATT	1519
55	OCTCCTTCCA GTTCCCTCTT TGATTTCCTT CTCATTGATC GGTTCTTTTT TCTTTTTTGC	1579
	TCTCCGTGCT CTCTTTTATT CGCCTTCCGT CTCCTGTCT CGTTTTCTCT TCACTTTTTT	1639
60	TTTTCATCTT CTCTCGGTCA ACTTGTCATT TAATCTCTCT AGGGTCTCAT GTCAACACGT	1699
	GCCAAGCATG TCATAAGTGT GCAGGGTGAT GTACAGTCAT TTGCCATCC CTCCTGCGAG	1759
	GGTCTCATCT ATCTTGCTTA TOGACTTTTC CTCTTTTTGA ATTCTCTGG AGTTTATCT	1819
65	TGGTATAAGC AATGGAGAAG AGCGCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAACTCG	1879
	AGG	1882

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Tyr Ala Asn Ile Leu Thr Ala Ile Pro Leu Glu Phe Thr Pro  
 1 5 10 15  
 Gln Asp Asp Ile Val Leu Leu Glu Pro Tyr His Tyr Leu Gly Lys Asn  
 20 25 30  
 Pro Gly Lys Glu Ile Arg Ser Gln Leu Ile Glu Ala Phe Asn Tyr Trp  
 35 40 45  
 Leu Asp Val Lys Lys Glu Asp Leu Glu Val Ile Gln Asn Val Val Gly  
 50 55 60  
 Met Leu His Thr Ala Ser Leu Leu Met Asp Asp Val Glu Asp Ser Ser  
 65 70 75 80  
 Val Leu Arg Arg Gly Ser Pro Val Ala His Leu Ile Tyr Gly Ile Pro  
 85 90 95  
 Gln Thr Ile Asn Thr Ala Asn Tyr Val Tyr Phe Leu Ala Tyr Gln Glu  
 100 105 110  
 Ile Phe Lys Leu Arg Pro Thr Pro Ile Pro Met Pro Val Ile Pro Pro  
 115 120 125  
 Ser Ser Ala Ser Leu Gln Ser Ser Val Ser Ser Ala Ser Ser Ser Ser  
 130 135 140  
 Ser Ala Ser Ser Glu Asn Gly Gly Thr Ser Thr Pro Asn Ser Gln Ile  
 145 150 155 160  
 Pro Phe Ser Lys Asp Thr Tyr Leu Asp Lys Val Ile Thr Asp Glu Met  
 165 170 175  
 Leu Ser Leu His Arg Gly Gln Gly Leu Glu Leu Phe Trp Arg Asp Ser  
 180 185 190  
 Leu Thr Cys Pro Ser Glu Glu Glu Tyr Val Lys Met Val Leu Gly Lys  
 195 200 205  
 Thr Gly Gly Leu Phe Arg Ile Ala Val Arg Leu Met Met Ala Lys Ser  
 210 215 220  
 Glu Cys Asp Ile Asp Phe Val Gln Leu Val Asn Leu Ile Ser Ile Tyr  
 225 230 235 240  
 Phe Gln Ile Arg Asp Asp Tyr Met Asn Leu Gln Ser Ser Glu Tyr Ala  
 245 250 255  
 His Asn Lys Asn Phe Ala Glu Asp Leu Thr Glu Gly Lys Phe Ser Phe  
 260 265 270  
 Pro Thr Ile His Ser Ile His Ala Asn Pro Ser Ser Arg Leu Val Ile  
 275 280 285  
 Asn Thr Leu Gln Lys Lys Ser Thr Ser Pro Glu Ile Leu His His Cys  
 290 295 300  
 Val Asn Tyr Met Arg Thr Glu Thr His Ser Phe Glu Tyr Thr Gln Glu

	305					310					315				320	
	Val	Leu	Asn	Thr	Leu	Ser	Gly	Ala	Leu	Glu	Arg	Glu	Leu	Gly	Arg	Leu
					325					330					335	
5	Gln	Gly	Glu	Phe	Ala	Glu	Ala	Asn	Ser	Arg	Met	Asp	Leu	Gly	Asp	Val
				340					345					350		
	Asp	Ser	Glu	Gly	Arg	Thr	Gly	Lys	Asn	Val	Lys	Leu	Glu	Ala	Ile	Leu
10			355					360					365			
	Lys	Lys	Leu	Ala	Asp	Ile	Pro	Leu								
		370					375									

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phaffia rhodozyma*

(ix) **FEATURE:**

(A) NAME/KEY: CDS

(B) LOCATION: 46..1794

(D) OTHER INFORMATION: /product= "PRcrTI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	CCTGCGCGAA	TCTAAGTTGA	CACATAACTC	TAGTATCTAT	ACTTCG	ATG GGA AAA	Met Gly Lys 1	54
45	GAA CAA GAT CAG GAT AAA CCC ACA GCT ATC ATC GTG GGA TGT GGT ATC Glu Gln Asp Gln Asp Lys Pro Thr Ala Ile Ile Val Gly Cys Gly Ile 5 10 15							102
50	GGT GGA ATC GCC ACT GCC GCT CGT CTT GCT AAA GAA GGT TTC CAG GTC Gly Gly Ile Ala Thr Ala Ala Arg Leu Ala Lys Glu Gly Phe Gln Val 20 25 30 35							150
55	ACG GTG TTC GAG AAG AAC GAC TAC TCC GGA GGT CGA TGC TCT TTA ATC Thr Val Phe Glu Lys Asn Asp Tyr Ser Gly Gly Arg Cys Ser Leu Ile 40 45 50							198
60	GAG CGA GAT GGT TAT CGA TTC GAT CAG GGG CCC AGT TTG CTG CTC TTG Glu Arg Asp Gly Tyr Arg Phe Asp Gln Gly Pro Ser Leu Leu Leu Leu 55 60 65							246
65	CCA GAT CTC TTC AAG CAG ACA TTC GAA GAT TTG GGA GAG AAG ATG GAA Pro Asp Leu Phe Lys Gln Thr Phe Glu Asp Leu Gly Glu Lys Met Glu 70 75 80							294
70	GAT TGG GTC GAT CTC ATC AAG TGT GAA CCC AAC TAT GTT TGC CAC TTC Asp Trp Val Asp Leu Ile Lys Cys Glu Pro Asn Tyr Val Cys His Phe 85 90 95							342
75	CAC GAT GAA GAG ACT TTC ACT TTT TCA ACC GAC ATG GCG TTG CTC AAG His Asp Glu Glu Thr Phe Thr Phe Ser Thr Asp Met Ala Leu Leu Lys 100 105 110 115 120							390



	100	105	110	115	
5	CGG GAA GTC GAG CGT TTT GAA GGC AAA GAT GGA TTT GAT CGG TTC TTG Arg Glu Val Glu Arg Phe Glu Gly Lys Asp Gly Phe Asp Arg Phe Leu	120	125	130	438
10	TCG TTT ATC CAA GAA GCC CAC AGA CAT TAC GAG CTT GCT GTC GTT CAC Ser Phe Ile Gln Glu Ala His Arg His Tyr Glu Leu Ala Val Val His	135	140	145	486
15	GTC CTG CAG AAG AAC TTC CCT GGC TTC GCA GCA TTC TTA CCG CTA CAG Val Leu Gln Lys Asn Phe Pro Gly Phe Ala Ala Phe Leu Arg Leu Gln	150	155	160	534
20	TTC ATT GGC CAA ATC CTG GCT CTT CAC CCC TTC GAG TCT ATC TGG ACA Phe Ile Gly Gln Ile Leu Ala Leu His Pro Phe Glu Ser Ile Trp Thr	165	170	175	582
25	AGA GTT TGT CGA TAT TTC AAG ACC GAC AGA TTA CGA AGA GTC TTC TCG Arg Val Cys Arg Tyr Phe Lys Thr Asp Arg Leu Arg Arg Val Phe Ser	180	185	190	630
30	TTT GCA GTG ATG TAC ATG GGT CAA AGC CCA TAC AGT GCG CCC GGA ACA Phe Ala Val Met Tyr Met Gly Gln Ser Pro Tyr Ser Ala Pro Gly Thr	200	205	210	678
35	TAT TCC TTG CTC CAA TAC ACC GAA TTG ACC GAG GGC ATC TGG TAT CCG Tyr Ser Leu Leu Gln Tyr Thr Glu Leu Thr Glu Gly Ile Trp Tyr Pro	215	220	225	726
40	AGA GGA GGC TTT TGG CAG GTT CCT AAT ACT CTT CTT CAG ATC GTC AAG Arg Gly Gly Phe Trp Gln Val Pro Asn Thr Leu Leu Gln Ile Val Lys	230	235	240	774
45	CGC AAC AAT CCC TCA GGC AAG TTC AAT TTC AAC GCT CCA GTT TCC CAG Arg Asn Asn Pro Ser Ala Lys Phe Asn Phe Asn Ala Pro Val Ser Gln	245	250	255	822
50	GTT CTT CTC TCT CCT GCC AAG GAC CGA GCG ACT GGT GTT CGA CTT GAA Val Leu Leu Ser Pro Ala Lys Asp Arg Ala Thr Gly Val Arg Leu Glu	260	265	270	870
55	TCC GGC GAG GAA CAT CAC GCC GAT GTT GTG ATT GTC AAT GCT GAC CTC Ser Gly Glu Glu His His Ala Asp Val Val Ile Val Asn Ala Asp Leu	280	285	290	918
60	GTT TAC GCC TCC GAG CAC TTG ATT CCT GAC GAT GCC AGA AAC AAG ATT Val Tyr Ala Ser Glu His Leu Ile Pro Asp Asp Ala Arg Asn Lys Ile	295	300	305	966
65	GGC CAA CTG GGT GAA GTC AAG AGA AGT TGG TGG GCT GAC TTA GTT GGT Gly Gln Leu Gly Glu Val Lys Arg Ser Trp Trp Ala Asp Leu Val Gly	310	315	320	1014
70	GGA AAG AAG CTC AAG GGA AGT TGC AGT AGT TTG AGC TTC TAC TGG AGC Gly Lys Lys Leu Lys Gly Ser Cys Ser Ser Leu Ser Phe Tyr Trp Ser	325	330	335	1062
75	ATG GAC CGA ATC GTG GAC GGT CTG GGC GGA CAC AAT ATC TTC TTG GCC Met Asp Arg Ile Val Asp Gly Leu Gly Gly His Asn Ile Phe Leu Ala	340	345	350	1110
80	GAG GAC TTC AAG GGA TCA TTC GAC ACA ATC TTC GAG GAG TTG GGT CTC Glu Asp Phe Lys Gly Ser Phe Asp Thr Ile Phe Glu Glu Leu Gly Leu	360	365	370	1158
85	CCA GCC GAT CCT TCC TTT TAC GTG AAC GTT CCC TCG CGA ATC GAT CCT Pro Ala Asp Pro Ser Phe Tyr Val Asn Val Pro Ser Arg Ile Asp Pro	375	380	385	1206

	TCT GGC GCT CCC GAA GGC AAA GAT GCT ATC GTC ATT CTT GTG CCG TGT	1254
	Ser Ala Ala Pro Glu Gly Lys Asp Ala Ile Val Ile Leu Val Pro Cys	
	390 395 400	
5	GGC CAT ATC GAC GCT TCG AAC CCT CAA GAT TAC AAC AAG CTT GTT GCT	1302
	Gly His Ile Asp Ala Ser Asn Pro Gln Asp Tyr Asn Lys Leu Val Ala	
	405 410 415	
10	CGG GCA AGG AAG TTT GTG ATC CAA ACG CTT TCC GCC AAG CTT GGA CTT	1350
	Arg Ala Arg Lys Phe Val Ile Gln Thr Leu Ser Ala Lys Leu Gly Leu	
	420 425 430 435	
15	CCC GAC TTT GAA AAA ATG ATT GTG GCA GAG AAG GTT CAC GAT GCT CCC	1398
	Pro Asp Phe Glu Lys Met Ile Val Ala Glu Lys Val His Asp Ala Pro	
	440 445 450	
	TCT TGG GAG AAA GAA TTT AAC CTC AAG GAC GGA AGC ATC TTG GGA CTG	1446
	Ser Trp Glu Lys Glu Phe Asn Leu Lys Asp Gly Ser Ile Leu Gly Leu	
	455 460 465	
20	GCT CAC AAC TTT ATG CAA GTT CTT GGT TTC AGG CCG AGC ACC AGA CAT	1494
	Ala His Asn Phe Met Gln Val Leu Gly Phe Arg Pro Ser Thr Arg His	
	470 475 480	
25	CCC AAG TAT GAC AAG TTG TTC TTT GTC GGG GCT TCG ACT CAT CCC GGA	1542
	Pro Lys Tyr Asp Lys Leu Phe Phe Val Gly Ala Ser Thr His Pro Gly	
	485 490 495	
30	ACT GGG GTT CCC ATC GTC TTG GCT GGA GCC AAG TTA ACT GCC AAC CAA	1590
	Thr Gly Val Pro Ile Val Leu Ala Gly Ala Lys Leu Thr Ala Asn Gln	
	500 505 510 515	
35	GTT CTC GAA TCC TTT GAC CGA TCC CCA GCT CCA GAT CCC AAT ATG TCA	1638
	Val Leu Glu Ser Phe Asp Arg Ser Pro Ala Pro Asp Pro Asn Met Ser	
	520 525 530	
	CTC TCC GTA CCA TAT GGA AAA CCT CTC AAA TCA AAT GGA ACG GGT ATC	1686
	Leu Ser Val Pro Tyr Gly Lys Pro Leu Lys Ser Asn Gly Thr Gly Ile	
	535 540 545	
40	GAT TCT CAG GTC CAG CTG AAG TTC ATG GAT TTG GAG AGA TGG GTA TAC	1734
	Asp Ser Gln Val Gln Leu Lys Phe Met Asp Leu Glu Arg Trp Val Tyr	
	550 555 560	
45	CTT TTG GTG TTG TTG ATT GGG GCC GTG ATC GCT CGA TCC GTT GGT GTT	1782
	Leu Leu Val Leu Leu Ile Gly Ala Val Ile Ala Arg Ser Val Gly Val	
	565 570 575	
50	CTT GCT TTC TGAAGCAAGA CAACGATCGT TTCTTAGAGT TTTTITTAGT	1831
	Leu Ala Phe	
	580	
	CTCTTCCTGT GTTCTCTCTA TATACATACT CTGCTCGTCT GTTCTCTTCT CGAGGGTTCC	1891
55	TCCTTACTTT GTGTCAGAGT CATACCGGT CTCTCTCAAC GTCGGTTTGA GGGCTAGACA	1951
	ATGTGTAGTC TCGAAATCTC CATCACTCA AGTCTGATGT TCATCATCTT TTTTATTGCT	2011
60	TGCAATATAC ATGACTGTTA TGGACCGAAA AAAAAAAAAA AAAAAAA	2058

## (2) INFORMATION FOR SEQ ID NO:17:

- 65 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 582 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Lys	Glu	Gln	Asp	Gln	Asp	Lys	Pro	Thr	Ala	Ile	Ile	Val	Gly	1	5	10	15
Cys	Gly	Ile	Gly	Gly	Ile	Ala	Thr	Ala	Ala	Arg	Leu	Ala	Lys	Glu	Gly	20	25	30	
Phe	Gln	Val	Thr	Val	Phe	Glu	Lys	Asn	Asp	Tyr	Ser	Gly	Gly	Arg	Cys	35	40	45	
Ser	Leu	Ile	Glu	Arg	Asp	Gly	Tyr	Arg	Phe	Asp	Gln	Gly	Pro	Ser	Leu	50	55	60	
Leu	Leu	Leu	Pro	Asp	Leu	Phe	Lys	Gln	Thr	Phe	Glu	Asp	Leu	Gly	Glu	65	70	75	80
Lys	Met	Glu	Asp	Trp	Val	Asp	Leu	Ile	Lys	Cys	Glu	Pro	Asn	Tyr	Val	85	90	95	
Cys	His	Phe	His	Asp	Glu	Glu	Thr	Phe	Thr	Phe	Ser	Thr	Asp	Met	Ala	100	105	110	
Leu	Leu	Lys	Arg	Glu	Val	Glu	Arg	Phe	Glu	Gly	Lys	Asp	Gly	Phe	Asp	115	120	125	
Arg	Phe	Leu	Ser	Phe	Ile	Gln	Glu	Ala	His	Arg	His	Tyr	Glu	Leu	Ala	130	135	140	
Val	Val	His	Val	Leu	Gln	Lys	Asn	Phe	Pro	Gly	Phe	Ala	Ala	Phe	Leu	145	150	155	160
Arg	Leu	Gln	Phe	Ile	Gly	Gln	Ile	Leu	Ala	Leu	His	Pro	Phe	Glu	Ser	165	170	175	
Ile	Trp	Thr	Arg	Val	Cys	Arg	Tyr	Phe	Lys	Thr	Asp	Arg	Leu	Arg	Arg	180	185	190	
Val	Phe	Ser	Phe	Ala	Val	Met	Tyr	Met	Gly	Gln	Ser	Pro	Tyr	Ser	Ala	195	200	205	
Pro	Gly	Thr	Tyr	Ser	Leu	Leu	Gln	Tyr	Thr	Glu	Leu	Thr	Glu	Gly	Ile	210	215	220	
Trp	Tyr	Pro	Arg	Gly	Gly	Phe	Trp	Gln	Val	Pro	Asn	Thr	Leu	Leu	Gln	225	230	235	240
Ile	Val	Lys	Arg	Asn	Asn	Pro	Ser	Ala	Lys	Phe	Asn	Phe	Asn	Ala	Pro	245	250	255	
Val	Ser	Gln	Val	Leu	Leu	Ser	Pro	Ala	Lys	Asp	Arg	Ala	Thr	Gly	Val	260	265	270	
Arg	Leu	Glu	Ser	Gly	Glu	Glu	His	His	Ala	Asp	Val	Val	Ile	Val	Asn	275	280	285	
Ala	Asp	Leu	Val	Tyr	Ala	Ser	Glu	His	Leu	Ile	Pro	Asp	Asp	Ala	Arg	290	295	300	
Asn	Lys	Ile	Gly	Gln	Leu	Gly	Glu	Val	Lys	Arg	Ser	Trp	Trp	Ala	Asp	305	310	315	320
Leu	Val	Gly	Gly	Lys	Lys	Leu	Lys	Gly	Ser	Cys	Ser	Ser	Leu	Ser	Phe	325	330	335	
Tyr	Trp	Ser	Met	Asp	Arg	Ile	Val	Asp	Gly	Leu	Gly	Gly	His	Asn	Ile	340	345	350	
Phe	Leu	Ala	Glu	Asp	Phe	Lys	Gly	Ser	Phe	Asp	Thr	Ile	Phe	Glu	Glu	355	360	365	

Leu Gly Leu Pro Ala Asp Pro Ser Phe Tyr Val Asn Val Pro Ser Arg  
 370 375 380  
 Ile Asp Pro Ser Ala Ala Pro Glu Gly Lys Asp Ala Ile Val Ile Leu  
 385 390 395 400  
 Val Pro Cys Gly His Ile Asp Ala Ser Asn Pro Gln Asp Tyr Asn Lys  
 405 410 415  
 10 Leu Val Ala Arg Ala Arg Lys Phe Val Ile Gln Thr Leu Ser Ala Lys  
 420 425 430  
 Leu Gly Leu Pro Asp Phe Glu Lys Met Ile Val Ala Glu Lys Val His  
 435 440 445  
 15 Asp Ala Pro Ser Trp Glu Lys Glu Phe Asn Leu Lys Asp Gly Ser Ile  
 450 455 460  
 Leu Gly Leu Ala His Asn Phe Met Gln Val Leu Gly Phe Arg Pro Ser  
 20 465 470 475 480  
 Thr Arg His Pro Lys Tyr Asp Lys Leu Phe Phe Val Gly Ala Ser Thr  
 485 490 495  
 25 His Pro Gly Thr Gly Val Pro Ile Val Leu Ala Gly Ala Lys Leu Thr  
 500 505 510  
 Ala Asn Gln Val Leu Glu Ser Phe Asp Arg Ser Pro Ala Pro Asp Pro  
 515 520 525  
 30 Asn Met Ser Leu Ser Val Pro Tyr Gly Lys Pro Leu Lys Ser Asn Gly  
 530 535 540  
 Thr Gly Ile Asp Ser Gln Val Gln Leu Lys Phe Met Asp Leu Glu Arg  
 35 545 550 555 560  
 Trp Val Tyr Leu Leu Val Leu Leu Ile Gly Ala Val Ile Ala Arg Ser  
 565 570 575  
 40 Val Gly Val Leu Ala Phe  
 580

45 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Phaffia rhodozyma

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 177..2198

(D) OTHER INFORMATION: /product= "PRcrTY"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACAAGAAGT GGACACAGAG AGATCTTTGC TGAAGAGTTG TATTCCAGAA AGGGAAAACA

60

70

	AAGGAAAGAA GCGCGAAGC ACATCACCA CTTACAGCAAG CCGGTCCAGC CCGATCTCGG	120
	ATAGACATCA TCTTACCCAA CTGGTATCAT CCCCACAGA TAGAGTTTTT GTGCA	176
5	ATG ACG GCT CTC GCA TAT TAC CAG ATC CAT CTG ATC TAT ACT CTC CCA Met Thr Ala Leu Ala Tyr Tyr Gln Ile His Leu Ile Tyr Thr Leu Pro 1 5 10 15	224
10	ATT CTT GGT CTT CTC GGC CTG CTC ACT TCC CCG ATT TTG ACA AAA TTT Ile Leu Gly Leu Leu Gly Leu Leu Thr Ser Pro Ile Leu Thr Lys Phe 20 25 30	272
15	GAC ATC TAC AAA ATA TCG ATC CTC GTA TTT ATT GCG TTT AGT GCA ACC Asp Ile Tyr Lys Ile Ser Ile Leu Val Phe Ile Ala Phe Ser Ala Thr 35 40 45	320
20	ACA CCA TGG GAC TCA TGG ATC ATC AGA AAT GGC GCA TGG ACA TAT CCA Thr Pro Trp Asp Ser Trp Ile Ile Arg Asn Gly Ala Trp Thr Tyr Pro 50 55 60	368
25	TCA GCG GAG AGT GGC CAA GGC GTG TTT GGA ACG TTT CTA GAT GTT CCA Ser Ala Glu Ser Gly Gln Gly Val Phe Gly Thr Phe Leu Asp Val Pro 65 70 75 80	416
30	TAT GAA GAG TAC GCT TTC TTT GTC ATT CAA ACC GTA ATC ACC GGC TTG Tyr Glu Glu Tyr Ala Phe Phe Val Ile Gln Thr Val Ile Thr Gly Leu 85 90 95	464
35	GTC TAC GTC TTG GCA ACT AGG CAC CTT CTC CCA TCT CTC GCG CTT CCC Val Tyr Val Leu Ala Thr Arg His Leu Leu Pro Ser Leu Ala Leu Pro 100 105 110	512
40	AAG ACT AGA TCG TCC GCC CTT TCT CTC GCG CTC AAG GCG CTC ATC CCT Lys Thr Arg Ser Ser Ala Leu Ser Leu Ala Leu Lys Ala Leu Ile Pro 115 120 125	560
45	CTG CCC ATT ATC TAC CTA TTT ACC GCT CAC CCC AGC CCA TCG CCC GAC Leu Pro Ile Ile Tyr Leu Phe Thr Ala His Pro Ser Pro Ser Pro Asp 130 135 140	608
50	CCG CTC GTG ACA GAT CAC TAC TTC TAC ATG CCG GCA CTC TCC TTA CTC Pro Leu Val Thr Asp His Tyr Phe Tyr Met Arg Ala Leu Ser Leu Leu 145 150 155 160	656
55	ATC ACC CCA CCT ACC ATG CTC TTG GCA GCA TTA TCA GGC GAA TAT GCT Ile Thr Pro Pro Thr Met Leu Leu Ala Ala Leu Ser Gly Glu Tyr Ala 165 170 175	704
60	TTC GAT TGG AAA AGT GGC CGA GCA AAG TCA ACT ATT GCA GCA ATC ATG Phe Asp Trp Lys Ser Gly Arg Ala Lys Ser Thr Ile Ala Ala Ile Met 180 185 190	752
65	ATC CCG ACG GTG TAT CTG ATT TGG GTA GAT TAT GTT GCT GTC GGT CAA Ile Pro Thr Val Tyr Leu Ile Trp Val Asp Tyr Val Ala Val Gly Gln 195 200 205	800
70	GAC TCT TGG TCG ATC AAC GAT GAG AAG ATT GTA GGG TGG AGG CTT GGA Asp Ser Trp Ser Ile Asn Asp Glu Lys Ile Val Gly Trp Arg Leu Gly 210 215 220	848
75	GGT GTA CTA CCC ATT GAG GAA GCT ATG TTC TTC TTA CTG ACG AAT CTA Gly Val Leu Pro Ile Glu Glu Ala Met Phe Phe Leu Leu Thr Asn Leu 225 230 235 240	896
80	ATG ATT GTT CTG GGT CTG TCT GCC TGC GAT CAT ACT CAG GCC CTA TAC Met Ile Val Leu Gly Leu Ser Ala Cys Asp His Thr Gln Ala Leu Tyr 245 250 255	944
85	CTG CTA CAC GGT CGA ACT ATT TAT GGC AAC AAA AAG ATG CCA TCT TCA Leu Leu His Gly Arg Thr Ile Tyr Gly Asn Lys Lys Met Pro Ser Ser 260 265 270	992

	260	265	270	
5	TTT CCC CTC ATT ACA CCG CCT GTG CTC TCC CTG TTT TTT AGC AGC CGA Phe Pro Leu Ile Thr Pro Pro Val Leu Ser Leu Phe Phe Ser Ser Arg 275 280 285	1040		
10	CCA TAC TCT TCT CAG CCA AAA CGT GAC TTG GAA CTG GCA GTC AAG TTG Pro Tyr Ser Ser Gln Pro Lys Arg Asp Leu Glu Leu Ala Val Lys Leu 290 295 300	1088		
15	TTG GAG AAA AAG AGC CCG AGC TTT TTT GTT GCC TCG GCT GGA TTT CCT Leu Glu Lys Lys Ser Arg Ser Phe Phe Val Ala Ser Ala Gly Phe Pro 305 310 315 320	1136		
20	AGC GAA GTT AGG GAG AGG CTG GTT GGA CTA TAC GCA TTC TGC CCG GTG Ser Glu Val Arg Glu Arg Leu Val Gly Leu Tyr Ala Phe Cys Arg Val 325 330 335	1184		
25	ACT GAT GAT CTT ATC GAC TCT CCT GAA GTA TCT TCC AAC CCG CAT GCC Thr Asp Asp Leu Ile Asp Ser Pro Glu Val Ser Ser Asn Pro His Ala 340 345 350	1232		
30	ACA ATT GAC ATG GTC TCC GAT TTT CTT ACC CTA CTA TTT GGG CCC CCG Thr Ile Asp Met Val Ser Asp Phe Leu Thr Leu Leu Phe Gly Pro Pro 355 360 365	1280		
35	CTA CAC CCT TCG CAA CCT GAC AAG ATC CTT TCT TCG CCT TTA CTT CCT Leu His Pro Ser Gln Pro Asp Lys Ile Leu Ser Ser Pro Leu Leu Pro 370 375 380	1328		
40	CCT TCG CAC CCT TCC CGA CCC ACG GGA ATG TAT CCC CTC CCG CCT CCT Pro Ser His Pro Ser Arg Pro Thr Gly Met Tyr Pro Leu Pro Pro Pro 385 390 395 400	1376		
45	CCT TCG CTC TCG CCT GCC GAG CTC GTT CAA TTC CTT ACC GAA AGG GTT Pro Ser Leu Ser Pro Ala Glu Leu Val Gln Phe Leu Thr Glu Arg Val 405 410 415	1424		
50	CCC GTT CAA TAC CAT TTC GCC TTC AGG TTG CTC GCT AAG TTG CAA GGG Pro Val Gln Tyr His Phe Ala Phe Arg Leu Leu Ala Lys Leu Gln Gly 420 425 430	1472		
55	CTG ATC CCT CGA TAC CCA CTC GAC GAA CTC CTT AGA GGA TAC ACC ACT Leu Ile Pro Arg Tyr Pro Leu Asp Glu Leu Leu Arg Gly Tyr Thr Thr 435 440 445	1520		
60	GAT CTT ATC TTT CCC TTA TCG ACA GAG GCA GTC CAG GCT CCG AAG ACG Asp Leu Ile Phe Pro Leu Ser Thr Glu Ala Val Gln Ala Arg Lys Thr 450 455 460	1568		
65	CCT ATC GAG ACC ACA GCT GAC TTG CTG GAC TAT GGT CTA TGT GTA GCA Pro Ile Glu Thr Thr Ala Asp Leu Leu Asp Tyr Gly Leu Cys Val Ala 465 470 475 480	1616		
70	GGC TCA GTC GCC GAG CTA TTG GTC TAT GTC TCT TGG GCA AGT GCA CCA Gly Ser Val Ala Glu Leu Leu Val Tyr Val Ser Trp Ala Ser Ala Pro 485 490 495	1664		
75	AGT CAG GTC CCT GCC ACC ATA GAA GAA AGA GAA GCT GTG TTA GTG GCA Ser Gln Val Pro Ala Thr Ile Glu Glu Arg Glu Ala Val Leu Val Ala 500 505 510	1712		
80	AGC CGA GAG ATG GGA ACT GCC CTT CAG TTG GTG AAC ATT GCT AGG GAC Ser Arg Glu Met Gly Thr Ala Leu Gln Leu Val Asn Ile Ala Arg Asp 515 520 525	1760		
85	ATT AAA GGG GAC GCA ACA GAA GGG AGA TTT TAC CTA CCA CTC TCA TTC Ile Lys Gly Asp Ala Thr Glu Gly Arg Phe Tyr Leu Pro Leu Ser Phe 530 535 540	1808		

	TTT GGT CTT CGG GAT GAA TCA AAG CTT GCG ATC CCG ACT GAT TGG ACG Phe Gly Leu Arg Asp Glu Ser Lys Leu Ala Ile Pro Thr Asp Trp Thr 545 550 555 560	1856
5	GAA CCT CGG CCT CAA GAT TTC GAC AAA CTC CTC AGT CTA TCT CCT TCG Glu Pro Arg Pro Gln Asp Phe Asp Lys Leu Leu Ser Leu Ser Pro Ser 565 570 575	1904
10	TCC ACA TTA CCA TCT TCA AAC GCC TCA GAA AGC TTC CCG TTC GAA TGG Ser Thr Leu Pro Ser Ser Asn Ala Ser Glu Ser Phe Arg Phe Glu Trp 580 585 590	1952
15	AAG ACG TAC TCG CTT CCA TTA GTC GCC TAC GCA GAG GAT CTT GCC AAA Lys Thr Tyr Ser Leu Pro Leu Val Ala Tyr Ala Glu Asp Leu Ala Lys 595 600 605	2000
20	CAT TCT TAT AAG GGA ATT GAC CGA CTT OCT ACC GAG GTT CAA GCG GGA His Ser Tyr Lys Gly Ile Asp Arg Leu Pro Thr Glu Val Gln Ala Gly 610 615 620	2048
25	ATG CGA GCG GCT TGC GCG AGC TAC CTA CTG ATC GGC CGA GAG ATC AAA Met Arg Ala Ala Cys Ala Ser Tyr Leu Leu Ile Gly Arg Glu Ile Lys 625 630 635 640	2096
	GTC GTT TGG AAA GGA GAC GTC GGA GAG AGA AGG ACA GTT GCC GGA TGG Val Val Trp Lys Gly Asp Val Gly Glu Arg Arg Thr Val Ala Gly Trp 645 650 655	2144
30	AGG AGA GTA CCG AAA GTC TTG AGT GTG GTC ATG AGC GGA TGG GAA GGG Arg Arg Val Arg Lys Val Leu Ser Val Val Met Ser Gly Trp Glu Gly 660 665 670	2192
35	CAG TAAGACAGCG GAAGAATACC GACAGACAAT GATGAGTGAG AATAAAATCA Gln	2245
	TCCTCAATCT TCTTCTCTCA GGTGCTCTTT TTTGTTTCT ATTATGACCA ACTCTAAAGG	2305
40	AACTGGCCCT GCAGATATTT CTCTTCCCC CATCTTCTC CTTCOCATCG TTTGTTCTTT	2365
	CCATTTTGT CGGTITACTA TGCAATTCT TTTTCTGCT TTTTCTTATC AATCTAGACA	2425
45	ATTCTATAGA TGTTTAGAAT TTATACAAAA AAAAAAAAAA AAAAA	2470

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Thr Ala Leu Ala Tyr Tyr Gln Ile His Leu Ile Tyr Thr Leu Pro 1 5 10 15	
Ile Leu Gly Leu Leu Gly Leu Leu Thr Ser Pro Ile Leu Thr Lys Phe 20 25 30	
Asp Ile Tyr Lys Ile Ser Ile Leu Val Phe Ile Ala Phe Ser Ala Thr 35 40 45	
Thr Pro Trp Asp Ser Trp Ile Ile Arg Asn Gly Ala Trp Thr Tyr Pro 50 55 60	
Ser Ala Glu Ser Gly Gln Gly Val Phe Gly Thr Phe Leu Asp Val Pro	

	65		70		75		80									
	Tyr	Glu	Glu	Tyr	Ala	Phe	Phe	Val	Ile	Gln	Thr	Val	Ile	Thr	Gly	Leu
					85					90					95	
5	Val	Tyr	Val	Leu	Ala	Thr	Arg	His	Leu	Leu	Pro	Ser	Leu	Ala	Leu	Pro
				100					105					110		
	Lys	Thr	Arg	Ser	Ser	Ala	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Leu	Ile	Pro
10			115					120					125			
	Leu	Pro	Ile	Ile	Tyr	Leu	Phe	Thr	Ala	His	Pro	Ser	Pro	Ser	Pro	Asp
		130					135					140				
15	Pro	Leu	Val	Thr	Asp	His	Tyr	Phe	Tyr	Met	Arg	Ala	Leu	Ser	Leu	Leu
	145					150					155					160
	Ile	Thr	Pro	Pro	Thr	Met	Leu	Leu	Ala	Ala	Leu	Ser	Gly	Glu	Tyr	Ala
20					165				170						175	
	Phe	Asp	Trp	Lys	Ser	Gly	Arg	Ala	Lys	Ser	Thr	Ile	Ala	Ala	Ile	Met
				180					185						190	
	Ile	Pro	Thr	Val	Tyr	Leu	Ile	Trp	Val	Asp	Tyr	Val	Ala	Val	Gly	Gln
25			195					200					205			
	Asp	Ser	Trp	Ser	Ile	Asn	Asp	Glu	Lys	Ile	Val	Gly	Trp	Arg	Leu	Gly
		210					215					220				
30	Gly	Val	Leu	Pro	Ile	Glu	Glu	Ala	Met	Phe	Phe	Leu	Leu	Thr	Asn	Leu
	225					230					235					240
	Met	Ile	Val	Leu	Gly	Leu	Ser	Ala	Cys	Asp	His	Thr	Gln	Ala	Leu	Tyr
35				245					250						255	
	Leu	Leu	His	Gly	Arg	Thr	Ile	Tyr	Gly	Asn	Lys	Lys	Met	Pro	Ser	Ser
			260						265					270		
	Phe	Pro	Leu	Ile	Thr	Pro	Pro	Val	Leu	Ser	Leu	Phe	Phe	Ser	Ser	Arg
40			275					280					285			
	Pro	Tyr	Ser	Ser	Gln	Pro	Lys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Lys	Leu
		290					295					300				
45	Leu	Glu	Lys	Lys	Ser	Arg	Ser	Phe	Phe	Val	Ala	Ser	Ala	Gly	Phe	Pro
	305					310					315					320
	Ser	Glu	Val	Arg	Glu	Arg	Leu	Val	Gly	Leu	Tyr	Ala	Phe	Cys	Arg	Val
50				325					330					335		
	Thr	Asp	Asp	Leu	Ile	Asp	Ser	Pro	Glu	Val	Ser	Ser	Asn	Pro	His	Ala
			340						345					350		
	Thr	Ile	Asp	Met	Val	Ser	Asp	Phe	Leu	Thr	Leu	Leu	Phe	Gly	Pro	Pro
55			355					360					365			
	Leu	His	Pro	Ser	Gln	Pro	Asp	Lys	Ile	Leu	Ser	Ser	Pro	Leu	Leu	Pro
		370					375					380				
60	Pro	Ser	His	Pro	Ser	Arg	Pro	Thr	Gly	Met	Tyr	Pro	Leu	Pro	Pro	Pro
	385					390					395					400
	Pro	Ser	Leu	Ser	Pro	Ala	Glu	Leu	Val	Gln	Phe	Leu	Thr	Glu	Arg	Val
65				405						410					415	
	Pro	Val	Gln	Tyr	His	Phe	Ala	Phe	Arg	Leu	Leu	Ala	Lys	Leu	Gln	Gly
			420					425					430			
	Leu	Ile	Pro	Arg	Tyr	Pro	Leu	Asp	Glu	Leu	Leu	Arg	Gly	Tyr	Thr	Thr
70			435					440					445			



Asp Leu Ile Phe Pro Leu Ser Thr Glu Ala Val Gln Ala Arg Lys Thr  
 450 455 460  
 Pro Ile Glu Thr Thr Ala Asp Leu Leu Asp Tyr Gly Leu Cys Val Ala  
 5 465 470 475 480  
 Gly Ser Val Ala Glu Leu Leu Val Tyr Val Ser Trp Ala Ser Ala Pro  
 485 490 495  
 10 Ser Gln Val Pro Ala Thr Ile Glu Glu Arg Glu Ala Val Leu Val Ala  
 500 505 510  
 Ser Arg Glu Met Gly Thr Ala Leu Gln Leu Val Asn Ile Ala Arg Asp  
 515 520 525  
 15 Ile Lys Gly Asp Ala Thr Glu Gly Arg Phe Tyr Leu Pro Leu Ser Phe  
 530 535 540  
 Phe Gly Leu Arg Asp Glu Ser Lys Leu Ala Ile Pro Thr Asp Trp Thr  
 20 545 550 555 560  
 Glu Pro Arg Pro Gln Asp Phe Asp Lys Leu Leu Ser Leu Ser Pro Ser  
 565 570 575  
 25 Ser Thr Leu Pro Ser Ser Asn Ala Ser Glu Ser Phe Arg Phe Glu Trp  
 580 585 590  
 Lys Thr Tyr Ser Leu Pro Leu Val Ala Tyr Ala Glu Asp Leu Ala Lys  
 595 600 605  
 30 His Ser Tyr Lys Gly Ile Asp Arg Leu Pro Thr Glu Val Gln Ala Gly  
 610 615 620  
 Met Arg Ala Ala Cys Ala Ser Tyr Leu Leu Ile Gly Arg Glu Ile Lys  
 35 625 630 635 640  
 Val Val Trp Lys Gly Asp Val Gly Glu Arg Arg Thr Val Ala Gly Trp  
 645 650 655  
 40 Arg Arg Val Arg Lys Val Leu Ser Val Val Met Ser Gly Trp Glu Gly  
 660 665 670

Gln

45

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 1165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Phaffia rhodozyma*  
 (ix) FEATURE:  
 65 (A) NAME/KEY: CDS  
 (B) LOCATION: 141..896  
 (D) OTHER INFORMATION: /product= "Pridi"  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

	CTTCTCTTTC CTGACCTCT TCGGCAGGCC GTTGAAGACT CGTTTACTCA TACCCACAT	60
	CTGCGATATA TCACCTTCCT CCTTCCAGAA CAGTTCCTGA GTCAACCGAA AAGAAAGAAG	120
5	GCAGAAGAAA TATATCTAG ATG TCC ATG CCC AAC ATT GTT CCC CCC GCC Met Ser Met Pro Asn Ile Val Pro Pro Ala 1 5 10	170
10	GAG GTC CGA ACC GAA GGA CTC AGT TTA GAA GAG TAC GAT GAG GAG CAG Glu Val Arg Thr Glu Gly Leu Ser Leu Glu Tyr Asp Glu Glu Gln 15 20 25	218
15	GTC AGG CTG ATG GAG GAG CGA TGT ATT CTT GTT AAC CCG GAC GAT GTG Val Arg Leu Met Glu Glu Arg Cys Ile Leu Val Asn Pro Asp Asp Val 30 35 40	266
20	GCC TAT GGA GAG GCT TCG AAA AAG ACC TGC CAC TTG ATG TCC AAC ATC Ala Tyr Gly Glu Ala Ser Lys Lys Thr Cys His Leu Met Ser Asn Ile 45 50 55	314
25	AAC GCG CCC AAG GAC CTC CTC CAC CGA GCA TTC TCC GTG TTT CTC TTC Asn Ala Pro Lys Asp Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe 60 65 70	362
30	CGC CCA TCG GAC GGA GCA CTC CTG CTT CAG CGA AGA GCG GAC GAG AAG Arg Pro Ser Asp Gly Ala Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys 75 80 85 90	410
35	ATT ACG TTC CCT GGA ATG TCG ACC AAC ACG TGT TGC AGT CAT CCT TTG Ile Thr Phe Pro Gly Met Trp Thr Asn Thr Cys Cys Ser His Pro Leu 95 100 105	458
40	AGC ATC AAG GGC GAG GTT GAA GAG GAG AAC CAG ATC GGT GTT CGA CGA Ser Ile Lys Gly Glu Val Glu Glu Asn Gln Ile Gly Val Arg Arg 110 115 120	506
45	GCT GCG TCC CGA AAG TTG GAG CAC GAG CTT GGC GTG CCT ACA TCG TCG Ala Ala Ser Arg Lys Leu Glu His Glu Leu Gly Val Pro Thr Ser Ser 125 130 135	554
50	ACT CCG CCC GAC TCG TTC ACC TAC CTC ACT AGG ATA CAT TAC CTC GCT Thr Pro Pro Asp Ser Phe Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala 140 145 150	602
55	CCG AGT GAC GGA CTC TGG GGA GAA CAC GAG ATC GAC TAC ATT CTC TTC Pro Ser Asp Gly Leu Trp Gly Glu His Glu Ile Asp Tyr Ile Leu Phe 155 160 165 170	650
60	TCA ACC ACA CCT ACA GAA CAC ACT GGA AAC CCT AAC GAA GTC TCT GAC Ser Thr Thr Pro Thr Glu His Thr Gly Asn Pro Asn Glu Val Ser Asp 175 180 185	698
65	ACT CGA TAT GTC ACC AAG CCC GAG CTC CAG GCG ATG TTT GAG GAC GAG Thr Arg Tyr Val Thr Lys Pro Glu Leu Gln Ala Met Phe Glu Asp Glu 190 195 200	746
70	TCT AAC TCA TTT ACC CCT TGG TTC AAA TTG ATT GCC CGA GAC TTC CTG Ser Asn Ser Phe Thr Pro Trp Phe Lys Leu Ile Ala Arg Asp Phe Leu 205 210 215	794
75	TTT GGC TGG TGG GAT CAA CTT CTC GCC AGA CGA AAT GAA AAG GGT GAG Phe Gly Trp Trp Asp Gln Leu Ala Arg Arg Asn Glu Lys Gly Glu 220 225 230	842
80	GTC GAT GCC AAA TCG TTG GAG GAT CTC TCG GAC AAC AAA GTC TGG AAG Val Asp Ala Lys Ser Leu Glu Asp Leu Ser Asp Asn Lys Val Trp Lys 235 240 245 250	890
85	ATG TAGTCGACC TTCTTCTGT ACAGTCATCT CAGTTCGCCT GTTGGTTGCT Met	943

TGCTTCTTGC TCTTCTTTCT ATATATCTTT TTTCTTGGCT GGGTAGACTT GATCTTTCTA 1003  
 CATAGCATAC GCATACATAC ATAAACTCTA TTTCTTGTTC TTTATCTCTC TTCTAAGGGA 1063  
 5 ATCTTCAAGA TCAATTCTTT TTTGGGCTAC AACATTTCAG ATCAATATTG CTTTTCAGAC 1123  
 TACAAAAAAA AAAAAAATAA ACTCGAGGGG GGGCCCGGTA CC 1165

10 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids  
 (B) TYPE: amino acid  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

20 Met Ser Met Pro Asn Ile Val Pro Pro Ala Glu Val Arg Thr Glu Gly  
 1 5 10 15  
 25 Leu Ser Leu Glu Glu Tyr Asp Glu Glu Gln Val Arg Leu Met Glu Glu  
 20 25 30  
 35 Arg Cys Ile Leu Val Asn Pro Asp Asp Val Ala Tyr Gly Glu Ala Ser  
 35 40 45  
 30 Lys Lys Thr Cys His Leu Met Ser Asn Ile Asn Ala Pro Lys Asp Leu  
 50 55 60  
 35 Leu His Arg Ala Phe Ser Val Phe Leu Phe Arg Pro Ser Asp Gly Ala  
 65 70 75 80  
 40 Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys Ile Thr Phe Pro Gly Met  
 85 90 95  
 45 Trp Thr Asn Thr Cys Cys Ser His Pro Leu Ser Ile Lys Gly Glu Val  
 100 105 110  
 50 Glu Glu Glu Asn Gln Ile Gly Val Arg Arg Ala Ala Ser Arg Lys Leu  
 115 120 125  
 55 Glu His Glu Leu Gly Val Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe  
 130 135 140  
 60 Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala Pro Ser Asp Gly Leu Trp  
 145 150 155 160  
 65 Gly Glu His Glu Ile Asp Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu  
 165 170 175  
 70 His Thr Gly Asn Pro Asn Glu Val Ser Asp Thr Arg Tyr Val Thr Lys  
 180 185 190  
 75 Pro Glu Leu Gln Ala Met Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro  
 195 200 205  
 80 Trp Phe Lys Leu Ile Ala Arg Asp Phe Leu Phe Gly Trp Trp Asp Gln  
 210 215 220  
 85 Leu Leu Ala Arg Arg Asn Glu Lys Gly Glu Val Asp Ala Lys Ser Leu  
 225 230 235 240  
 90 Glu Asp Leu Ser Asp Asn Lys Val Trp Lys Met  
 245 250

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*
- (B) STRAIN: CBS 6938

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 941..966

## (ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 967..1077

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1078..1284

## (ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 1285..1364

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1365..1877

## (ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 1878..1959

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1960..2202

## (ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 2203..2292

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 2293..3325

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(941..966, 1078..1284, 1365..1877, 1960..2202, 2293..3325)
- (D) OTHER INFORMATION: /product= "PRGertB GB"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGAATTCCAG TTTTGCCCTTT GACGAGAAAG GACACTGGGT TGGAAAGAGA AGATGGTACG	60
TTCTTCTCCA CCTTGAATGT GTTGCTTACT AGACATGTTT GACACGCTAA TGCATTTCCT	120
TCCACTTTGA CTTTTGAAGT ATGGTGGTTG GCGATCCCC AAAATCAATTA GCTTCTACTT	180
CAGCTCAATTA CCTGATCTC ATCTTACTAC CAGGTGTTC ATTCTACCT ACGGCTCTTT	240

	CTTTGTTCTC TOGACTGGGC CATGGAAAAG GATATTACGA TAAATACATC ACTCAGTATC	300
	GGTCGATCTG TGCAGGCAAG AATCGACCCG TCCGAAGCTG AGTACGGCTC TTCTCTTTTC	360
5	TCGATACCCA ACGGAGCCTA TTTTGTGACA GAAGGATGAG ACTATCCAAC AGCTCAAACA	420
	AACTAAGCTT CTTGATTAAAT CACCCGCTCA ACTTATTGCT CAACTCAGTT GGACTGGCGC	480
	TGAAGAACA GTTCTTAGAC AAAACATGG TCCCTATAGG AGAATGGGAT GCGAATCTGG	540
10	ATGAAGTGT TGGTGGAGAT CAOGTGAGGA CATATCCGA GGACAATTAA CTACTTAAGA	600
	TATATACATG ATTTATGTGG ATCGGCATCC AGCCGGGGAT TGATCGGCTG ATGGCCGGAA	660
15	ATGTGATGAT GGTGAAACT CGATCTCTCT TTTTGTGTC ATCTTCTCAT CCTCTTCTC	720
	TCTTTCTACT GACATCCATC TCCAACGTG TAGATCAGTT CGGAAACAAG AAGTGGACAC	780
	AGAGAGATCT TTGCTGAAGA GTTGTATTCC AGAAAGGGAA AACAAAGGAA AGAAGCGCCG	840
20	AAGCACATCA CCAACTTCAG CAAGCCGGTC CAGCCCGATC TCGGATAGAC ATCATCTTAC	900
	CCAACTCGTA TCATCCCCAA CAGATAGAGT TTTTGTGCA ATG ACG GCT CTC GCA	955
25		Met Thr Ala Leu Ala 1 5
	TAT TAC CAG AT GTTGTCTCC ATACCTCTTC TTGTTTTGC ACACCACTCA	1006
	Tyr Tyr Gln Ile	
30	TGTGTGCATA TGIGTGTGG TCCCTCCAAA TCTTTCAATG ACTAACATCT TTACCGTGCT	1066
	CTTCTCTTTA G C CAT CTG ATC TAT ACT CTC CCA ATT CTT GGT CTT CTC	1114
	His Leu Ile Tyr Thr Leu Pro Ile Leu Gly Leu Leu	
35	10 15 20	
	GGC CTG CTC ACT TCC CCG ATT TTG ACA AAA TTT GAC ATC TAC AAA ATA	1162
	Gly Leu Leu Thr Ser Pro Ile Leu Thr Lys Phe Asp Ile Tyr Lys Ile	
	25 30 35	
40	TCG ATC CTC GTA TTT ATT GCG TTT AGT GCA ACC ACA CCA TGG GAC TCA	1210
	Ser Ile Leu Val Phe Ile Ala Phe Ser Ala Thr Thr Pro Trp Asp Ser	
	40 45 50	
45	TGG ATC ATC AGA AAT GGC GCA TGG ACA TAT CCA TCA GCG GAG AGT GGC	1258
	Trp Ile Ile Arg Asn Gly Ala Trp Thr Tyr Pro Ser Ala Glu Ser Gly	
	55 60 65	
	CAA GGC GTG TTT GGA ACG TTT CTA GA GTTAGTGGAC CGTAATACT	1304
50	Gln Gly Val Phe Gly Thr Phe Leu Asp	
	70 75	
	CCTAGCCGCG CGTCGTTTCC GCGATTACAT TTAACATCTG AATTTATCCC TGATCAACAG	1364
55	T GTT CCA TAT GAA GAG TAC GCT TTC TTT GTC ATT CAA ACC GTA ATC	1410
	Val Pro Tyr Glu Glu Tyr Ala Phe Phe Val Ile Gln Thr Val Ile	
	80 85 90	
	ACC GGC TTG GTC TAC GTC TTG GCA ACT AGG CAC CTT CTC CCA TCT CTC	1458
60	Thr Gly Leu Val Tyr Val Leu Ala Thr Arg His Leu Leu Pro Ser Leu	
	95 100 105	
	GCG CTT CCC AAG ACT AGA TCG TCC GGC CTT TCT CTC GCG CTC AAG GCG	1506
	Ala Leu Pro Lys Thr Arg Ser Ser Ala Leu Ser Leu Ala Leu Lys Ala	
65	110 115 120 125	
	CTC ATC CCT CTG CCC ATT ATC TAC CTA TTT ACC GCT CAC CCC AGC CCA	1554
	Leu Ile Pro Leu Pro Ile Ile Tyr Leu Phe Thr Ala His Pro Ser Pro	
	130 135 140	
70		

	TCG CCC GAC CCG CTC GTG ACA GAT CAC TAC TTC TAC ATG CCG GCA CTC	1602
	Ser Pro Asp Pro Leu Val Thr Asp His Tyr Phe Tyr Met Arg Ala Leu	
	145 150 155	
5	TCC TTA CTC ATC ACC CCA CCT ACC ATG CTC TTG GCA GCA TTA TCA GGC	1650
	Ser Leu Leu Ile Thr Pro Pro Thr Met Leu Leu Ala Ala Leu Ser Gly	
	160 165 170	
10	GAA TAT GCT TTC GAT TGG AAA AGT GGC CGA GCA AAG TCA ACT ATT GCA	1698
	Glu Tyr Ala Phe Asp Trp Lys Ser Gly Arg Ala Lys Ser Thr Ile Ala	
	175 180 185	
15	GCA ATC ATG ATC CCG ACG GTG TAT CTG ATT TGG GTA GAT TAT GTT GCT	1746
	Ala Ile Met Ile Pro Thr Val Tyr Leu Ile Trp Val Asp Tyr Val Ala	
	190 195 200 205	
20	GTC GGT CAA GAC TCT TGG TCG ATC AAC GAT GAG AAG ATT GTA GGG TGG	1794
	Val Gly Gln Asp Ser Trp Ser Ile Asn Asp Glu Lys Ile Val Gly Trp	
	210 215 220	
25	AGG CTT GGA GGT GTA CTA CCC ATT GAG GAA GCT ATG TTC TTC TTA CTG	1842
	Arg Leu Gly Gly Val Leu Pro Ile Glu Glu Ala Met Phe Phe Leu Leu	
	225 230 235	
30	ACG AAT CTA ATG ATT GTT CTG GGT CTG TCT GCC TG GTAAGTTGAT	1887
	Thr Asn Leu Met Ile Val Leu Gly Leu Ser Ala Cys	
	240 245	
35	CTCATCTCT CTTCCTTTGG TGAAAAAGC TGTTTGGCTG ATTGCTGCGA ACTCACCCT	1947
	CGGAATCTGT AG C GAT CAT ACT CAG GCC CTA TAC CTG CTA CAC GGT CGA	1996
	Asp His Thr Gln Ala Leu Tyr Leu Leu His Gly Arg	
	250 255 260	
40	ACT ATT TAT GGC AAC AAA AAG ATG CCA TCT TCA TTT CCC CTC ATT ACA	2044
	Thr Ile Tyr Gly Asn Lys Lys Met Pro Ser Ser Phe Pro Leu Ile Thr	
	265 270 275	
45	CCG CCT GTG CTC TCC CTG TTT TTT AGC AGC CGA CCA TAC TCT TCT CAG	2092
	Pro Pro Val Leu Ser Leu Phe Phe Ser Ser Arg Pro Tyr Ser Ser Gln	
	280 285 290	
50	CCA AAA CGT GAC TTG GAA CTG GCA GTC AAG TTG TTG GAG AAA AAG AGC	2140
	Pro Lys Arg Asp Leu Glu Leu Ala Val Lys Leu Leu Glu Lys Lys Ser	
	295 300 305	
55	CGG AGC TTT TTT GTT GCC TCG GCT GGA TTT CCT AGC GAA GTT AGG GAG	2188
	Arg Ser Phe Phe Val Ala Ser Ala Gly Phe Pro Ser Glu Val Arg Glu	
	310 315 320 325	
60	AGG CTG GTT GGA CT GIGAGCAGGC ATTCTTTAGG TTGTTGGGT CTTTCACCTT	2242
	Arg Leu Val Gly Leu	
	330	
65	CATGIGCATT CGCTGATCAG TTTTCTTGGT GATCCGGGAC CTGCATACAG A TAC GCA	2299
	Tyr Ala	
70	TTC TGC CCG GTG ACT GAT GAT CTT ATC GAC TCT CCT GAA GTA TCT TCC	2347
	Phe Cys Arg Val Thr Asp Asp Leu Ile Asp Ser Pro Glu Val Ser Ser	
	335 340 345	
75	AAC CCG CAT GGC ACA ATT GAC ATG GTC TCC GAT TTT CTT ACC CTA CTA	2395
	Asn Pro His Ala Thr Ile Asp Met Val Ser Asp Phe Leu Thr Leu Leu	
	350 355 360	
80	TTT GGG CCC CCG CTA CAC CCT TCG CAA CCT GAC AAG ATC CTT TCT TCG	2443
	Phe Gly Pro Pro Leu His Pro Ser Gln Pro Asp Lys Ile Leu Ser Ser	
	365 370 375 380	

	CCT TTA CTT CCT CCT TCG CAC CCT TCC CGA CCC ACG GGA ATG TAT CCC	2491
	Pro Leu Leu Pro Pro Ser His Pro Ser Arg Pro Thr Gly Met Tyr Pro	
	385 390 395	
5	CTC CCG CCT CCT CCT TCG CTC TCG CCT GCC GAG CTC GTT CAA TTC CTT	2539
	Leu Pro Pro Pro Pro Ser Leu Ser Pro Ala Glu Leu Val Gln Phe Leu	
	400 405 410	
10	ACC GAA AGG GTT CCC GTT CAA TAC CAT TTC GCC TTC AGG TTG CTC GCT	2587
	Thr Glu Arg Val Pro Val Gln Tyr His Phe Ala Phe Arg Leu Leu Ala	
	415 420 425	
15	AAG TTG CAA GGG CTG ATC CCT CGA TAC CCA CTC GAC GAA CTC CTT AGA	2635
	Lys Leu Gln Gly Leu Ile Pro Arg Tyr Pro Leu Asp Glu Leu Leu Arg	
	430 435 440	
20	GGA TAC ACC ACT GAT CTT ATC TTT CCC TTA TCG ACA GAG GCA GTC CAG	2683
	Gly Tyr Thr Thr Asp Leu Ile Phe Pro Leu Ser Thr Glu Ala Val Gln	
	445 450 455 460	
25	GCT CGG AAG ACG CCT ATC GAG ACC ACA GCT GAC TTG CTG GAC TAT GGT	2731
	Ala Arg Lys Thr Pro Ile Glu Thr Thr Ala Asp Leu Leu Asp Tyr Gly	
	465 470 475	
30	CTA TGT GTA GCA GGC TCA GTC GCC GAG CTA TTG GTC TAT GTC TCT TGG	2779
	Leu Cys Val Ala Gly Ser Val Ala Glu Leu Leu Val Tyr Val Ser Trp	
	480 485 490	
35	GCA AGT GCA CCA AGT CAG GTC CCT GCC ACC ATA GAA GAA AGA GAA GCT	2827
	Ala Ser Ala Pro Ser Gln Val Pro Ala Thr Ile Glu Glu Arg Glu Ala	
	495 500 505	
40	GTG TTA GTG GCA AGC CGA GAG ATG GGA ACT GCC CTT CAG TTG GTG AAC	2875
	Val Leu Val Ala Ser Arg Glu Met Gly Thr Ala Leu Gln Leu Val Asn	
	510 515 520	
45	ATT GCT AGG GAC ATT AAA GGG GAC GCA ACA GAA GGG AGA TTT TAC CTA	2923
	Ile Ala Arg Asp Ile Lys Gly Asp Ala Thr Glu Gly Arg Phe Tyr Leu	
	525 530 535 540	
50	CCA CTC TCA TTC TTT GGT CTT CGG GAT GAA TCA AAG CTT GCG ATC CCG	2971
	Pro Leu Ser Phe Phe Gly Leu Arg Asp Glu Ser Lys Leu Ala Ile Pro	
	545 550 555	
55	ACT GAT TGG ACG GAA CCT CGG CCT CAA GAT TTC GAC AAA CTC CTC AGT	3019
	Thr Asp Trp Thr Glu Pro Arg Pro Gln Asp Phe Asp Lys Leu Leu Ser	
	560 565 570	
60	CTA TCT CCT TCG TCC ACA TTA CCA TCT TCA AAC GCC TCA GAA AGC TTC	3067
	Leu Ser Pro Ser Ser Thr Leu Pro Ser Ser Asn Ala Ser Glu Ser Phe	
	575 580 585	
65	CGG TTC GAA TGG AAG ACG TAC TCG CTT CCA TTA GTC GCC TAC GCA GAG	3115
	Arg Phe Glu Trp Lys Thr Tyr Ser Leu Pro Leu Val Ala Tyr Ala Glu	
	590 595 600	
70	GAT CTT GCC AAA CAT TCT TAT AAG GGA ATT GAC CGA CTT CCT ACC GAG	3163
	Asp Leu Ala Lys His Ser Tyr Lys Gly Ile Asp Arg Leu Pro Thr Glu	
	605 610 615 620	
75	GTT CAA GCG GGA ATG CGA GCG GCT TGC GCG AGC TAC CTA CTG ATC GGC	3211
	Val Gln Ala Gly Met Arg Ala Ala Cys Ala Ser Tyr Leu Leu Ile Gly	
	625 630 635	
80	CGA GAG ATC AAA GTC GTT TCG AAA GGA GAC GTC CGA GAG AGA AGG ACA	3259
	Arg Glu Ile Lys Val Val Trp Lys Gly Asp Val Gly Glu Arg Arg Thr	
	640 645 650	
85	GTT GCC GGA TGG AGG AGA GTA CCG AAA GTC TTG AGT GTG GTC ATG AGC	3307

Val Ala Gly Trp Arg Arg Val Arg Lys Val Leu Ser Val Val Met Ser  
 655 660 665

GGA TGG GAA GGG CAG TAAGACAGCG GAAGAATACC GACAGACAAT GATGAGTGAG 3362  
 5 Gly Trp Glu Gly Gln  
 670

AATAAAATCA TCCTCAATCT TCCTCTCTCTA GGTCCTCTTT TTGTGTTTCT ATTATGACCA 3422

10 ACTCTAAAGG AACTGGCCCT GCAGATATTT CTCCTCCCCC CATCTTCTCT CTTTCCATCG 3482

TTGTCTCTTT CCAATTTTGT CGGTTTACTA TGCAATCTCT TTTTCTTGCT TTTTCTTATC 3542

AATCTAGA 3550

15

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 673 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Thr Ala Leu Ala Tyr Tyr Gln Ile His Leu Ile Tyr Thr Leu Pro  
 1 5 10 15

30 Ile Leu Gly Leu Leu Gly Leu Leu Thr Ser Pro Ile Leu Thr Lys Phe  
 20 25 30

Asp Ile Tyr Lys Ile Ser Ile Leu Val Phe Ile Ala Phe Ser Ala Thr  
 35 40 45

Thr Pro Trp Asp Ser Trp Ile Ile Arg Asn Gly Ala Trp Thr Tyr Pro  
 50 55 60

40 Ser Ala Glu Ser Gly Gln Gly Val Phe Gly Thr Phe Leu Asp Val Pro  
 65 70 75 80

Tyr Glu Glu Tyr Ala Phe Phe Val Ile Gln Thr Val Ile Thr Gly Leu  
 85 90 95

45 Val Tyr Val Leu Ala Thr Arg His Leu Leu Pro Ser Leu Ala Leu Pro  
 100 105 110

50 Lys Thr Arg Ser Ser Ala Leu Ser Leu Ala Leu Lys Ala Leu Ile Pro  
 115 120 125

Leu Pro Ile Ile Tyr Leu Phe Thr Ala His Pro Ser Pro Ser Pro Asp  
 130 135 140

55 Pro Leu Val Thr Asp His Tyr Phe Tyr Met Arg Ala Leu Ser Leu Leu  
 145 150 155 160

Ile Thr Pro Pro Thr Met Leu Leu Ala Ala Leu Ser Gly Glu Tyr Ala  
 165 170 175

60 Phe Asp Trp Lys Ser Gly Arg Ala Lys Ser Thr Ile Ala Ala Ile Met  
 180 185 190

Ile Pro Thr Val Tyr Leu Ile Trp Val Asp Tyr Val Ala Val Gly Gln  
 195 200 205

65 Asp Ser Trp Ser Ile Asn Asp Glu Lys Ile Val Gly Trp Arg Leu Gly  
 210 215 220

70 Gly Val Leu Pro Ile Glu Glu Ala Met Phe Phe Leu Leu Thr Asn Leu



	225		230		235		240
	Met	Ile	Val	Leu	Gly	Leu	Tyr
				245		250	255
5	Leu	Leu	His	Gly	Arg	Thr	Ile
				260		265	270
	Phe	Pro	Leu	Ile	Thr	Pro	Pro
10			275			280	
	Pro	Tyr	Ser	Ser	Gln	Pro	Lys
						295	
	Leu	Glu	Lys	Lys	Ser	Arg	Ser
15						310	
	Ser	Glu	Val	Arg	Glu	Arg	Leu
						325	
20	Asp	Asp	Leu	Ile	Asp	Ser	Pro
							340
	Ile	Asp	Met	Val	Ser	Asp	Phe
25							355
	His	Pro	Ser	Gln	Pro	Asp	Lys
							370
30	Ser	His	Pro	Ser	Arg	Pro	Thr
							385
	Ser	Leu	Ser	Pro	Ala	Glu	Leu
							405
35	Val	Gln	Tyr	His	Phe	Ala	Phe
							420
	Ile	Pro	Arg	Tyr	Pro	Leu	Asp
40							435
	Leu	Ile	Phe	Pro	Leu	Ser	Thr
							450
45	Ile	Glu	Thr	Thr	Ala	Asp	Leu
							465
	Ser	Val	Ala	Glu	Leu	Leu	Val
							485
50	Gln	Val	Pro	Ala	Thr	Ile	Glu
							500
	Arg	Glu	Met	Gly	Thr	Ala	Leu
55							515
	Lys	Gly	Asp	Ala	Thr	Glu	Gly
							530
60	Gly	Leu	Arg	Asp	Glu	Ser	Lys
							545
	Pro	Arg	Pro	Gln	Asp	Phe	Asp
							565
65	Thr	Leu	Pro	Ser	Ser	Asn	Ala
							580
	Thr	Tyr	Ser	Leu	Pro	Leu	Val
70							595

Ser Tyr Lys Gly Ile Asp Arg Leu Pro Thr Glu Val Gln Ala Gly Met  
610 615 620

Arg Ala Ala Cys Ala Ser Tyr Leu Leu Ile Gly Arg Glu Ile Lys Val  
5 625 630 635 640

Val Trp Lys Gly Asp Val Gly Glu Arg Arg Thr Val Ala Gly Trp Arg  
645 650 655

10 Arg Val Arg Lys Val Leu Ser Val Val Met Ser Gly Trp Glu Gly Gln  
660 665 670

15

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 570 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Phaffia rhodozyma
- (ix) FEATURE:  
35 (A) NAME/KEY: CDS  
(B) LOCATION: 24..500  
(D) OTHER INFORMATION: /product= "PRcDNA10"

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AACACTTGGT TAGTTTCGAC GAC ATG CAG ATC TTC GTA AAG ACC CTC ACG	50
Met Gln Ile Phe Val Lys Thr Leu Thr	
1 5	
GGT AAG ACC ATC ACC CTT GAG GTG GAG TCT TCT GAC ACC ATC GAC AAC	98
Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn	
10 15 20 25	
GTC AAG GCC AAG ATC CAG GAC AAG GAA GGA ATT CCC CCT GAT CAG CAG	146
Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln	
30 35 40	
CGA CTT ATC TTC GCC GGT AAG CAG CTC GAG GAT GGC CGA ACC CTT TCG	194
Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser	
45 50 55	
GAT TAC AAC ATC CAG AAA GAG TCC ACC CTC CAC CTC GTC CTT AGG TTG	242
Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu	
60 65 70	
CGA GGA GGA GCC AAG AAG CGA AAG AAG AAG CAG TAC ACT ACC CCC AAG	290
Arg Gly Gly Ala Lys Lys Arg Lys Lys Lys Gln Tyr Thr Thr Pro Lys	
75 80 85	
AAG ATC AAG CAC AAG CGA AAG AAG GTC AAG ATG GCT ATT CTT AAG TAC	338
Lys Ile Lys His Lys Arg Lys Lys Val Lys Met Ala Ile Leu Lys Tyr	
90 95 100 105	
TAC AAG GTC GAC TCT GAT GGA AAG ATC AAG CGA CTT CGT CGA GAG TGC	386

Tyr Lys Val Asp Ser Asp Gly Lys Ile Lys Arg Leu Arg Arg Glu Cys  
 110 115 120  
 CCC CAG CCC CAG TGC GGA GCT GGT ATC TTC ATG GCT TTC CAC TCC AAC 434  
 5 Pro Gln Pro Gln Cys Gly Ala Gly Ile Phe Met Ala Phe His Ser Asn  
 125 130 135  
 CGA CAG ACT TGC GGA AAG TGT GGT CTT ACC TAC ACC TTC GCC GAG GGA 482  
 10 Arg Gln Thr Cys Gly Lys Cys Gly Leu Thr Tyr Thr Phe Ala Glu Gly  
 140 145 150  
 ACC CAG CCC TCT GCT TAGATCATCA ATCGTTTGTT CCGAGCGAT CTTTGAGTCT 537  
 Thr Gln Pro Ser Ala  
 155  
 15 TTGTTACATT CTCAAAAAA AAAAAAAA AAA 570

## (2) INFORMATION FOR SEQ ID NO:25:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  
 30 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
 1 5 10 15  
 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
 20 25 30  
 35 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45  
 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 40 50 55 60  
 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ala Lys Lys Arg  
 65 70 75 80  
 45 Lys Lys Lys Gln Tyr Thr Thr Pro Lys Lys Ile Lys His Lys Arg Lys  
 85 90 95  
 Lys Val Lys Met Ala Ile Leu Lys Tyr Tyr Lys Val Asp Ser Asp Gly  
 100 105 110  
 50 Lys Ile Lys Arg Leu Arg Arg Glu Cys Pro Gln Pro Gln Cys Gly Ala  
 115 120 125  
 Gly Ile Phe Met Ala Phe His Ser Asn Arg Gln Thr Cys Gly Lys Cys  
 55 130 135 140  
 Gly Leu Thr Tyr Thr Phe Ala Glu Gly Thr Gln Pro Ser Ala  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:26:

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 70

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phaffia rhodozyma*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..278

(D) OTHER INFORMATION: /product= "PRcDNA11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

15 TTTACACACA AACCTTAACT ACCTTTTCAA CAACAAATCA CACCTAAGCT TACATC          56
    ATG GAG TCC ATC AAG ACC TCG ATT TCC AAC GCC GCC AAC TAC GCT TCT          104
    Met Glu Ser Ile Lys Thr Ser Ile Ser Asn Ala Ala Asn Tyr Ala Ser
20   1             5             10             15
    GAG ACT GTC AAC CAG GCC ACT AGC GCC ACC TCC AAG GAG GCC AAC AAG          152
    Glu Thr Val Asn Gln Ala Thr Ser Ala Thr Ser Lys Glu Ala Asn Lys
        20             25             30
25   GAG GTT GCC AAG GAC TCC AAT GCC GGA GTT GGA ACC CGA ATC AAC GCC          200
    Glu Val Ala Lys Asp Ser Asn Ala Gly Val Gly Thr Arg Ile Asn Ala
        35             40             45
30   GGA ATT GAT GCT CTT GGA GAC AAG GCC GAC GAG ACT TCG TCT GAT GCC          248
    Gly Ile Asp Ala Leu Gly Asp Lys Ala Asp Glu Thr Ser Ser Asp Ala
        50             55             60
35   AAG TCC AAG GCC TAC AAG CAG AAC ATC TAAGTTATTT AGATAGTCGT          295
    Lys Ser Lys Ala Tyr Lys Gln Asn Ile
        65             70
40   CCATATTT          303

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

35 Met Glu Ser Ile Lys Thr Ser Ile Ser Asn Ala Ala Asn Tyr Ala Ser
    1             5             10             15
    Glu Thr Val Asn Gln Ala Thr Ser Ala Thr Ser Lys Glu Ala Asn Lys
        20             25             30
60   Glu Val Ala Lys Asp Ser Asn Ala Gly Val Gly Thr Arg Ile Asn Ala
        35             40             45
    Gly Ile Asp Ala Leu Gly Asp Lys Ala Asp Glu Thr Ser Ser Asp Ala
        50             55             60
65   Lys Ser Lys Ala Tyr Lys Gln Asn Ile
        65             70

```

(2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 3..227  
 (D) OTHER INFORMATION: /product= "PRcDNA18"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

AC CCT TCC ATC GAG TCT GAG GCC CGA CAA CAC AAG CTC AAG AGG CTT      47
Pro Ser Ile Glu Ser Glu Ala Arg Gln His Lys Leu Lys Arg Leu
   1             5             10             15

GTG CAG AGC CCC AAC TCT TTC TTC ATG GAC GTC AAG TGC CCT GGT TGC      95
Val Gln Ser Pro Asn Ser Phe Phe Met Asp Val Lys Cys Pro Gly Cys
          20             25             30

TTC CAG ATC ACC ACC GTG TTC TCG CAC GCT TCC ACT GCC GTT CAG TGT      143
Phe Gln Ile Thr Thr Val Phe Ser His Ala Ser Thr Ala Val Gln Cys
          35             40             45

GGA TCG TGC CAG ACC ATC CTC TGC CAG CCC CGG GGA GGA AAG GCT CGA      191
Gly Ser Cys Gln Thr Ile Leu Cys Gln Pro Arg Gly Gly Lys Ala Arg
          50             55             60

CTT ACC GAG GGA TGC TCT TTC CGA CGA AAG AAC TAAGTTTCTG TTATCGGATG      244
Leu Thr Glu Gly Cys Ser Phe Arg Arg Lys Asn
          65             70             75

ATGCATTCAA ATAAAAGTCA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG GCGCGGTACC      304
CAA                                                                307

```

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Pro Ser Ile Glu Ser Glu Ala Arg Gln His Lys Leu Lys Arg Leu Val
   1             5             10             15

Gln Ser Pro Asn Ser Phe Phe Met Asp Val Lys Cys Pro Gly Cys Phe
          20             25             30

Gln Ile Thr Thr Val Phe Ser His Ala Ser Thr Ala Val Gln Cys Gly
          35             40             45

```

Ser Cys Gln Thr Ile Leu Cys Gln Pro Arg Gly Gly Lys Ala Arg Leu  
50 55 60

Thr Glu Gly Cys Ser Phe Arg Arg Lys Asn  
65 70

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Phaffia rhodozyma*
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 30..359  
 (D) OTHER INFORMATION: /product= "PrdDNA35"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTCAGCTCCG GCTTAAATCG ATTGGTACA ATG TCT GAA CTC GCC GCC TCC TAC	53
Met Ser Glu Leu Ala Ala Ser Tyr	
1 5	
GCC GCT CTT ATC CTC GCC GAC GAG GGT ATT GAG ATC ACC TCT GAG AAG	101
Ala Ala Leu Ile Leu Ala Asp Glu Gly Ile Glu Ile Thr Ser Glu Lys	
10 15 20	
CTC GTC ACT CTC ACC ACC GCC GCC AAG GTT GAG CTT GAG CCC ATC TGG	149
Leu Val Thr Leu Thr Thr Ala Ala Lys Val Glu Leu Glu Pro Ile Trp	
25 30 35 40	
GCC ACT CTC CTT GCC AAG GCC CTC GAG GGA AAG AAC GTC AAG GAG TTG	197
Ala Thr Leu Leu Ala Lys Ala Leu Glu Gly Lys Asn Val Lys Glu Leu	
45 50 55	
CTT TCC AAC GTC GGA TCC GGA GCC GGA GGA GCT GCC CCC GCC GCC GCC	245
Leu Ser Asn Val Gly Ser Gly Ala Gly Gly Ala Ala Pro Ala Ala Ala	
60 65 70	
GTC GCC GGT GGA GCT TCC GCT GAC GCC TCT GCC CCC GCT GAG GAG AAG	293
Val Ala Gly Gly Ala Ser Ala Asp Ala Ser Ala Pro Ala Glu Glu Lys	
75 80 85	
AAG GAG GAG AAG GCT GAG GAC AAG GAG GAG TCT GAC GAC GAC ATG GGT	341
Lys Glu Lys Ala Glu Asp Lys Glu Glu Ser Asp Asp Met Gly	
90 95 100	
TTC GGA CTT TTC GAT TAAACTCCCT CGCCTAAAAA CCGTTTCTT CAACCCCTC	396
Phe Gly Leu Phe Asp	
105 110	
TCGTGGCATC GTTCACTCGA CCGCTGGT TGTGTGCTT TCCACAGAA TTTTGTCTT	456
GTCGTGTTTC CCAATNGGAT TTCCTTGAAA TGANGTTCC CAATTG	502

(2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ser Glu Leu Ala Ala Ser Tyr Ala Ala Leu Ile Leu Ala Asp Glu  
 1 5 10 15  
 Gly Ile Glu Ile Thr Ser Glu Lys Leu Val Thr Leu Thr Thr Ala Ala  
 20 25 30  
 Lys Val Glu Leu Glu Pro Ile Trp Ala Thr Leu Leu Ala Lys Ala Leu  
 35 40 45  
 Glu Gly Lys Asn Val Lys Glu Leu Leu Ser Asn Val Gly Ser Gly Ala  
 50 55 60  
 Gly Gly Ala Ala Pro Ala Ala Ala Val Ala Gly Gly Ala Ser Ala Asp  
 65 70 75 80  
 Ala Ser Ala Pro Ala Glu Glu Lys Lys Glu Glu Lys Ala Glu Asp Lys  
 85 90 95  
 Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu Phe Asp  
 100 105

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Phaffia rhodozyma

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 7..282  
 (D) OTHER INFORMATION: /product= "PrDNA38"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCAAG ATG ACC AAA GGT ACC TCC TCT TTC GGT AAG CGA CAC ACC AAG 48  
 Met Thr Lys Gly Thr Ser Ser Phe Gly Lys Arg His Thr Lys  
 1 5 10  
 ACC CAC ACC ATC TGC CGA CGA TGT GGT AAC AGG GCT TTC CAC AGG CAG 96  
 Thr His Thr Ile Cys Arg Arg Cys Gly Asn Arg Ala Phe His Arg Gln  
 15 20 25 30  
 AAG AAG ACC TGT GCC CAG TGT GGA TAC CCT GCC GCC AAG ATG CGA AGC 144  
 Lys Lys Thr Cys Ala Gln Cys Gly Tyr Pro Ala Ala Lys Met Arg Ser  
 35 40 45  
 TTC AAC TGG GGA GAG AAG GCC AAG AGG AGA AAG ACC ACC GGT ACC GGT 192  
 Phe Asn Trp Gly Glu Lys Ala Lys Arg Arg Lys Thr Thr Gly Thr Gly

50 55 60

CGA ATG CAG CAC CTC AAG GAC GTC TCT CGA CGA TTC AAG AAC GGC TTC 240  
 Arg Met Gln His Leu Lys Asp Val Ser Arg Arg Phe Lys Asn Gly Phe  
 65 70 75

CGA GAG GGA ACT TCC GCC ACC AAG AAG GTC AAG GCC GAG TAATCGGTTT 289  
 Arg Glu Gly Thr Ser Ala Thr Lys Lys Val Lys Ala Glu  
 80 85 90

10 ATCCATCACC TGGTGATCAG GCGGGTAAT AATCTTTTGT TAGAGACTAT CCATGTTCTG 349

CTGCCGCATC AAACAAAAAA AAAAAAAAAA AA 381

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Thr Lys Gly Thr Ser Ser Phe Gly Lys Arg His Thr Lys Thr His  
 1 5 10 15

Thr Ile Cys Arg Arg Cys Gly Asn Arg Ala Phe His Arg Gln Lys Lys  
 20 25 30

Thr Cys Ala Gln Cys Gly Tyr Pro Ala Ala Lys Met Arg Ser Phe Asn  
 35 40 45

Trp Gly Glu Lys Ala Lys Arg Arg Lys Thr Thr Gly Thr Gly Arg Met  
 50 55 60

Gln His Leu Lys Asp Val Ser Arg Arg Phe Lys Asn Gly Phe Arg Glu  
 65 70 75 80

Gly Thr Ser Ala Thr Lys Lys Val Lys Ala Glu  
 85 90

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 19..321  
 (D) OTHER INFORMATION: /product= "PRcDNA46"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:



	CTCAAGAAGA AACTCGCC ATG CCT ACC CGA TTC TCC AAC ACC CGA AAG CAC	51
	Met Pro Thr Arg Phe Ser Asn Thr Arg Lys His	
	1 5 10	
5	AGA GGA CAC GTC TCT GCC GGT CAC GGT CGT GTG GGA AAG CAC AGA AAG	99
	Arg Gly His Val Ser Ala Gly His Gly Arg Val Gly Lys His Arg Lys	
	15 20 25	
10	CAC CCA GGA GGA CGA GGT CTT GCT GGA GGA CAG CAC CAC CAC CGA ACC	147
	His Pro Gly Gly Arg Gly Leu Ala Gly Gly Gln His His His Arg Thr	
	30 35 40	
15	AAC TTC GAT AAG TAC CAC CCT GGA TAC TTC GGA AAG GTC GGA ATG AGG	195
	Asn Phe Asp Lys Tyr His Pro Gly Tyr Phe Gly Lys Val Gly Met Arg	
	45 50 55	
20	CAC TTC CAC CTT ACC CGA NAC TCT TCC TGG TGC CCT ACC GTC AAC ATT	243
	His Phe His Leu Thr Arg Xaa Ser Ser Trp Cys Pro Thr Val Asn Ile	
	60 65 70 75	
25	GAC NAG CTC TGG ACT CTC GTC CCC GCT GAG GAG AAG AAG GAC TTC CCC	291
	Asp Xaa Leu Trp Thr Leu Val Pro Ala Glu Glu Lys Lys Asp Phe Pro	
	80 85 90	
30	AAC CAG GCT CGA CCT CGT CCC CGT TGT TGACACTTTG GCTCTCGGTT	338
	Asn Gln Ala Arg Pro Arg Pro Arg Cys	
	95 100	
35	ACGGCAATGT TCTTGGCAAG GGTCTACTTC CCCAGATCCC TTTAATCGTC AAGGCCCGAT	398
	TGTTTCCGC TCTTGGCCGAG AANAANATCN ANGANGCTGG TTGGAATTCC TCTCCCTTT	458
	GTCCCCCCN TAANG	473

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

	Met Pro Thr Arg Phe Ser Asn Thr Arg Lys His Arg Gly His Val Ser	
	1 5 10 15	
50	Ala Gly His Gly Arg Val Gly Lys His Arg Lys His Pro Gly Gly Arg	
	20 25 30	
55	Gly Leu Ala Gly Gly Gln His His His Arg Thr Asn Phe Asp Lys Tyr	
	35 40 45	
	His Pro Gly Tyr Phe Gly Lys Val Gly Met Arg His Phe His Leu Thr	
	50 55 60	
60	Arg Xaa Ser Ser Trp Cys Pro Thr Val Asn Ile Asp Xaa Leu Trp Thr	
	65 70 75 80	
	Leu Val Pro Ala Glu Lys Lys Asp Phe Pro Asn Gln Ala Arg Pro	
	85 90 95	
65	Arg Pro Arg Cys	
	100	

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 18..453  
 (D) OTHER INFORMATION: /product= "PRcDNA64"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

25	AAGACTCGTC GTTCAGC ATG TCC TCC GTC AAA GCC ACC AAA GGA AAG GGT	50
	Met Ser Ser Val Lys Ala Thr Lys Gly Lys Gly	
	1 5 10	
30	CCC GCC GCC TCG GCT GAT GTT AAG GCC AAG GCC GCC AAG AAG GCT GCC	98
	Pro Ala Ala Ser Ala Asp Val Lys Ala Lys Ala Ala Lys Lys Ala Ala	
	15 20 25	
35	CTC AAG GGT ACT CAG TCT ACT TCC ACC AGG AAG GTC CGA ACT TCG GTC	146
	Leu Lys Gly Thr Gln Ser Thr Ser Thr Arg Lys Val Arg Thr Ser Val	
	30 35 40	
40	TCT TTC CAC CGA CCC AAG ACT CTC CGA CTT CCC CGA GCT CCC AAG TAC	194
	Ser Phe His Arg Pro Lys Thr Leu Arg Leu Pro Arg Ala Pro Lys Tyr	
	45 50 55	
45	CCC CGA AAG TCG GTC CCT CAC GCC CCT CGA ATG GAT GAG TTC CGA ACT	242
	Pro Arg Lys Ser Val Pro His Ala Pro Arg Met Asp Glu Phe Arg Thr	
	60 65 70 75	
50	ATC ATC CAC CCC TTG GCT ACC GAG TCC GCC ATG AAG AAG ATT GAG GAG	290
	Ile Ile His Pro Leu Ala Thr Glu Ser Ala Met Lys Lys Ile Glu Glu	
	80 85 90	
55	CAC AAC ACC CTT GTG TTC ATC GTC GAT GTC AAG TCC AAC AAG CGA CAG	338
	His Asn Thr Leu Val Phe Ile Val Asp Val Lys Ser Asn Lys Arg Gln	
	95 100 105	
60	ATC AAG GAC GCC GTC AAG AAG CTC TAC GAG GTC GAT ACC GTC CAC NTC	386
	Ile Lys Asp Ala Val Lys Lys Leu Tyr Glu Val Asp Thr Val His Xaa	
	110 115 120	
65	AAC NCC TTG ATC ACC CCC GCC GGA AGG AAG AAG CTT ACG TCC GAC TTA	434
	Asn Xaa Leu Ile Thr Pro Ala Gly Arg Lys Lys Leu Thr Ser Asp Leu	
	125 130 135	
70	CCC CCG ACC ACG ACG CTC T TAACGTTGCC AACAGGCGG GCTACATCTA	483
	Pro Pro Thr Thr Thr Leu	
	140 145	
75	ATCGACTCCA TCCCTTGGAT CGGTTGAGTT GTTTGGTTTG CATCCGGTTT CAGAGTTTGA	543
	CGACCTTGAA ACTCNAANAC TTTGGATGCA TGTTTGAAAT TCTCNAATA AAAAAAAAAA	603
	AAAAA	608

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Met Ser Ser Val Lys Ala Thr Lys Gly Lys Gly Pro Ala Ala Ser Ala
 1           5           10           15
Asp Val Lys Ala Lys Ala Ala Lys Lys Ala Ala Leu Lys Gly Thr Gln
15          20          25          30
Ser Thr Ser Thr Arg Lys Val Arg Thr Ser Val Ser Phe His Arg Pro
20          35          40          45
Lys Thr Leu Arg Leu Pro Arg Ala Pro Lys Tyr Pro Arg Lys Ser Val
25          50          55          60
Pro His Ala Pro Arg Met Asp Glu Phe Arg Thr Ile Ile His Pro Leu
30          65          70          75          80
Ala Thr Glu Ser Ala Met Lys Lys Ile Glu Glu His Asn Thr Leu Val
35          85          90          95
Phe Ile Val Asp Val Lys Ser Asn Lys Arg Gln Ile Lys Asp Ala Val
40          100         105         110
Lys Lys Leu Tyr Glu Val Asp Thr Val His Xaa Asn Xaa Leu Ile Thr
45          115         120         125
Pro Ala Gly Arg Lys Lys Leu Thr Ser Asp Leu Pro Pro Thr Thr Thr
50          130         135         140
Leu
55          145

```

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 81..416  
 (D) OTHER INFORMATION: /product= "PRC1NA68"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

CTTTGAACCT CCAACCTCGG CATCAAGCAC TAGTCAGCCT CGGCTTAAAT CGATTGTTGT      60
AGCCTTTTCAA ACTGGTAAAA ATG AAG CAC ATC GCC GCT TAC TTG CTC CTC      110
Met Lys His Ile Ala Ala Tyr Leu Leu Leu

```

		1							5						10		
5	GCC ACC GGT GGA AAC NCC TCC CCC TCT GCC GCC GAT GTC AAG GCC CTC															158	
	Ala Thr Gly Gly Asn Xaa Ser Pro Ser Ala Ala Asp Val Lys Ala Leu	15							20						25		
	CTT GCC ACC GTC GAC ATC GAG GCT GAT GAC GCC CGA CTT GAG ACC CTC															206	
	Leu Ala Thr Val Asp Ile Glu Ala Asp Asp Ala Arg Leu Glu Thr Leu	30						35						40			
10	ATC TCC GAG CTT AAC GGC AAG GAC TTG AAC ACC CTC ATC GCT GAG GGA															254	
	Ile Ser Glu Leu Asn Gly Lys Asp Leu Asn Thr Leu Ile Ala Glu Gly	45					50						55				
15	TCC GCC AAG CTC GCT TCC GTC CCC TCC GGA GGA GCC GCC TCT TCC GCT															302	
	Ser Ala Lys Leu Ala Ser Val Pro Ser Gly Gly Ala Ala Ser Ser Ala	60				65						70					
20	GCC CCC GCC GCC GCT GGA GGA GCC GCC GCC CCT GCC GCT GAG GAT AAG															350	
	Ala Pro Ala Ala Ala Gly Gly Ala Ala Ala Pro Ala Ala Glu Asp Lys	75			80					85					90		
25	AAG GAG GAG AAG GTC GAG GAC AAG GAG GAG TCT GAC GAC GAC ATG GGT															398	
	Lys Glu Glu Lys Val Glu Asp Lys Glu Glu Ser Asp Asp Asp Met Gly		95					100						105			
30	TTC GGA CTT TTC GAT TAAACTCCTT ACACCTTTTT CAAACTCTTC GTTGGCTOGA															453	
	Phe Gly Leu Phe Asp	110															
	GGGGGGGGCC GGT															466	

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

45	Met Lys His Ile Ala Ala Tyr Leu Leu Leu Ala Thr Gly Gly Asn Xaa	1	5	10	15
50	Ser Pro Ser Ala Ala Asp Val Lys Ala Leu Leu Ala Thr Val Asp Ile	20	25	30	
55	Glu Ala Asp Asp Ala Arg Leu Glu Thr Leu Ile Ser Glu Leu Asn Gly	35	40	45	
60	Lys Asp Leu Asn Thr Leu Ile Ala Glu Gly Ser Ala Lys Leu Ala Ser	50	55	60	
65	Val Pro Ser Gly Gly Ala Ala Ser Ser Ala Ala Pro Ala Ala Ala Gly	65	70	75	80
70	Gly Ala Ala Ala Pro Ala Ala Glu Asp Lys Lys Glu Glu Lys Val Glu	85	90	95	
75	Asp Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu Phe Asp	100	105	110	

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phaffia rhodozyma*

(ix) FEATURE:

15 (A) NAME/KEY: CDS

(B) LOCATION: 49..501

(D) OTHER INFORMATION: /product= "PRcDNA73"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CITCCTCCCG TCAAGGCAAA CCTTCAGAAT CCTCTCAAGT CATTCAAC ATG GGA CGA	57
Met Gly Arg	
1	
25 GTC CGC ACC AAA ACC GTC AAG CGA GCT TCG CGA GTG ATG ATC GAG AAG	105
Val Arg Thr Lys Thr Val Lys Arg Ala Ser Arg Val Met Ile Glu Lys	
5 10 15	
30 TTC TAC CCT CGA CTC ACT CTT GAT TTC CAC ACC AAC AAG CGA ATC GCC	153
Phe Tyr Pro Arg Leu Thr Leu Asp Phe His Thr Asn Lys Arg Ile Ala	
20 25 30 35	
35 GAC GAG GTT GCC ATC ATC CCC TCC AAG CGA CTT CGA AAC AAG ATC GCT	201
Asp Glu Val Ala Ile Ile Pro Ser Lys Arg Leu Arg Asn Lys Ile Ala	
40 45 50	
40 GGG TTC ACT ACC CAC TTG ATG AAG CGA ATC CAG AAG GGA CCC GTT CGA	249
Gly Phe Thr Thr His Leu Met Lys Arg Ile Gln Lys Gly Pro Val Arg	
55 60 65	
45 GGT ATC TCC TTC AAG CTT CAG GAG GAG GAG CGA GAG AGG AAG GAT CAG	297
Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg Lys Asp Gln	
70 75 80	
50 TAC GTT CCT GAG GTC TCC GCC CTT GCC GCC CCT GAG CTG GGT TTG GAG	345
Tyr Val Pro Glu Val Ser Ala Leu Ala Ala Pro Glu Leu Gly Leu Glu	
85 90 95	
55 GTT GAC CCC GAC ACC AAG GAT CTT CTC CGA TCC CTT GGC ATG GAC TCC	393
Val Asp Pro Asp Thr Lys Asp Leu Leu Arg Ser Leu Gly Met Asp Ser	
100 105 110 115	
60 ATC AAC GTC CAG GTC TCC GCT CCT ATC TCT TCC TAC GCT GCC CCC GAG	441
Ile Asn Val Gln Val Ser Ala Pro Ile Ser Ser Tyr Ala Ala Pro Glu	
120 125 130	
65 CGA GGT CCC CGA GGT GCC GGA CGA NGT GGA CGA ATC GTC CCC GGA GCT	489
Arg Gly Pro Arg Gly Ala Gly Arg Xaa Gly Arg Ile Val Pro Gly Ala	
135 140 145	
70 GGC CGA TAC TAAGTGTTTT CTCAACCAN GGGATATTTG ATNATTGCT	538
Gly Arg Tyr	
150	
AGGCTTGAAA TTTTITATC ATTCTTCCTA TA	570

(2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ala Ser Arg Val Met  
 1 5 10 15  
 Ile Glu Lys Phe Tyr Pro Arg Leu Thr Leu Asp Phe His Thr Asn Lys  
 20 25 30  
 Arg Ile Ala Asp Glu Val Ala Ile Ile Pro Ser Lys Arg Leu Arg Asn  
 35 40 45  
 Lys Ile Ala Gly Phe Thr Thr His Leu Met Lys Arg Ile Gln Lys Gly  
 50 55 60  
 Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg  
 65 70 75 80  
 Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Ala Ala Pro Glu Leu  
 85 90 95  
 Gly Leu Glu Val Asp Pro Asp Thr Lys Asp Leu Leu Arg Ser Leu Gly  
 100 105 110  
 Met Asp Ser Ile Asn Val Gln Val Ser Ala Pro Ile Ser Ser Tyr Ala  
 115 120 125  
 Ala Pro Glu Arg Gly Pro Arg Gly Ala Gly Arg Xaa Gly Arg Ile Val  
 130 135 140  
 Pro Gly Ala Gly Arg Tyr  
 145 150

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phaffia rhodozyma*

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 13..324  
 (D) OTHER INFORMATION: /product= "PrCINA76"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCATCATCCA AC ATG CCT CCC AAA GTC AAG GCC AAG ACC GGT GTC GGT 48  
 Met Pro Pro Lys Val Lys Ala Lys Thr Gly Val Gly  
 1 5 10  
 AAG ACC CAG AAG AAG AAG TGG TCC AAG GGA AAG GTG AAG GAC AAG 96

Lys Thr Gln Lys Lys Lys Lys Trp Ser Lys Gly Lys Val Lys Asp Lys  
 15 20 25  
 GCC GCC CAC CAC GTC GTT GTT GAT CAG GCC ACT TAC GAC AAG ATC GTT 144  
 5 Ala Ala His His Val Val Val Asp Gln Ala Thr Tyr Asp Lys Ile Val  
 30 35 40  
 AAG GAG GTC CCC ACC TAC AAG TTG ATC TCC CAG TCT ATC TTG ATT GAC 192  
 10 Lys Glu Val Pro Thr Tyr Lys Leu Ile Ser Gln Ser Ile Leu Ile Asp  
 45 50 55 60  
 CGA CAC AAG GTT AAC GGT TCC GTC GCC CGA GCC GCT ATC CGA CAC CTT 240  
 Arg His Lys Val Asn Gly Ser Val Ala Arg Ala Ala Ile Arg His Leu  
 65 70 75  
 15 GCC AAG GAG GGA TCC ATC AAG AAG ATT GTC CAC CAC AAC GGA CAG TGG 288  
 Ala Lys Glu Gly Ser Ile Lys Lys Ile Val His His Asn Gly Gln Trp  
 80 85 90  
 20 ATC TAC ACC CGA GCC ACT GCC GCT CCT GAC GCA TAAATCTGAT GGATTTCATG 341  
 Ile Tyr Thr Arg Ala Thr Ala Ala Pro Asp Ala  
 95 100  
 25 GATCTTGAAA AATAAAAAA AAAAAAAA AA 373

## (2) INFORMATION FOR SEQ ID NO:43:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- 35 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

40 Met Pro Pro Lys Val Lys Ala Lys Thr Gly Val Gly Lys Thr Gln Lys 15  
 1 5 10 15  
 Lys Lys Lys Trp Ser Lys Gly Lys Val Lys Asp Lys Ala Ala His His  
 20 25 30  
 45 Val Val Val Asp Gln Ala Thr Tyr Asp Lys Ile Val Lys Glu Val Pro  
 35 40 45  
 Thr Tyr Lys Leu Ile Ser Gln Ser Ile Leu Ile Asp Arg His Lys Val  
 50 55 60  
 50 Asn Gly Ser Val Ala Arg Ala Ala Ile Arg His Leu Ala Lys Glu Gly  
 65 70 75 80  
 Ser Ile Lys Lys Ile Val His His Asn Gly Gln Trp Ile Tyr Thr Arg  
 55 85 90 95  
 Ala Thr Ala Ala Pro Asp Ala  
 100

60

## (2) INFORMATION FOR SEQ ID NO:44:

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 514 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

- 70 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Phaffia rhodozyma*

(ix) FEATURE:  
(A) NAME/KEY: CDS  
10 (B) LOCATION: 13..435  
(D) OTHER INFORMATION: /product= "PRcDNA78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

15 AAAAAAGCCA AT ATG CTT ATC TCT AAA CAG AAC AGG AGG GCC ATC TTC 48  
Met Leu Ile Ser Lys Gln Asn Arg Arg Ala Ile Phe  
1 5 10

20 GAG AAC CTC TTC AAG GAG GGA GTT GCC GTC GCC GCC AAG GAC TTC AAC 96  
Glu Asn Leu Phe Lys Glu Gly Val Ala Val Ala Ala Lys Asp Phe Asn  
15 20 25

25 GCT GCC ACC CAC CCC GAG ATT GAG GGT GTC TCC AAC CTT GAG GTC ATC 144  
Ala Ala Thr His Pro Glu Ile Glu Gly Val Ser Asn Leu Glu Val Ile  
30 35 40

30 AAG GCC ATG CAG TCT TTG ACC TCC AAG GGA TAC GTG AAG ACC CAG TTC 192  
Lys Ala Met Gln Ser Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe  
45 50 55 60

35 TCG TGG CAG TAC TAC TAC TAC ACC CTC ACC CCT GAG GGT CTT GAC TAC 240  
Ser Trp Gln Tyr Tyr Tyr Tyr Thr Leu Thr Pro Glu Gly Leu Asp Tyr  
65 70 75

40 CTC CGA GAG TTC CTC CAC CTT CCC TCC GAG ATT GTC CCC AAC ACT CTC 288  
Leu Arg Glu Phe Leu His Leu Pro Ser Glu Ile Val Pro Asn Thr Leu  
80 85 90

45 AAG CGA CCC ACC CGA CCT GCC AAG GCC CAG GGT CCC GGA GGT GCC TAC 336  
Lys Arg Pro Thr Arg Pro Ala Lys Ala Gln Gly Pro Gly Gly Ala Tyr  
95 100 105

50 CGA GCT CCC CGA GCC GAG GGT GCC GGT CGA GGA GAG TAC CGA CGA CGA 384  
Arg Ala Pro Arg Ala Glu Gly Ala Gly Arg Gly Glu Tyr Arg Arg Arg  
110 115 120

55 GAG GAC GGT GCC GGT GCC TTC GGT GCC GGT CGA GGT GGA CCC CGA GCT 432  
Glu Asp Gly Ala Gly Ala Phe Gly Ala Gly Arg Gly Gly Pro Arg Ala  
125 130 135 140

TAAATCCAG AGCTTTTCTT TTGTGCTTG CTGGGACTAT GGCAATGATGA GCTGGCTTGC 492

AGAAAAAAAAAAAAAAAAAA AA 514

## (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Leu Ile Ser Lys Gln Asn Arg Arg Ala Ile Phe Glu Asn Leu Phe  
1 5 10 15



Lys Glu Gly Val Ala Val Ala Ala Lys Asp Phe Asn Ala Ala Thr His  
 20 25 30

Pro Glu Ile Glu Gly Val Ser Asn Leu Glu Val Ile Lys Ala Met Gln  
 5 35 40 45

Ser Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr  
 50 55 60

Tyr Tyr Tyr Thr Leu Thr Pro Glu Gly Leu Asp Tyr Leu Arg Glu Phe  
 10 65 70 75 80

Leu His Leu Pro Ser Glu Ile Val Pro Asn Thr Leu Lys Arg Pro Thr  
 85 90 95

Arg Pro Ala Lys Ala Gln Gly Pro Gly Gly Ala Tyr Arg Ala Pro Arg  
 15 100 105 110

Ala Glu Gly Ala Gly Arg Gly Glu Tyr Arg Arg Arg Glu Asp Gly Ala  
 20 115 120 125

Gly Ala Phe Gly Ala Gly Arg Gly Gly Pro Arg Ala  
 130 135 140

25

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (ii) MOLECULE TYPE: cDNA

35

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

40

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Phaffia rhodozyma

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 30..308  
 (D) OTHER INFORMATION: /product= "PRcDNA85"

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

50

CTCCCTCAAG AAATCAACCA CGCACATC ATG TCC AAG CGA ACC AAG AAA GTT 53  
 Met Ser Lys Arg Thr Lys Lys Val  
 1 5

GGA ATC ACC GGA AAG TAC GGA GTC CGA TAC GGA GCT TCC CTC CGA AAG 101  
 Gly Ile Thr Gly Lys Tyr Gly Val Arg Tyr Gly Ala Ser Leu Arg Lys  
 10 15 20

ACC GTC AAG AAG NTG GAG GTC TGG CAG CAC GGT ACC TAC ACC TGT GAC 149  
 Thr Val Lys Lys Xaa Glu Val Trp Gln His Gly Thr Tyr Thr Cys Asp  
 25 30 35 40

TTC TGC GGA AAG GAC GCC GTC AAG CGA ACC GCT GTT GGT ATC TGG AAG 197  
 Phe Cys Gly Lys Asp Ala Val Lys Arg Thr Ala Val Gly Ile Trp Lys  
 45 50 55

TGC CGA GGA TGC CGA AAG ACC ACC GCC GGT GGT GCT TGG CAG CTT CAG 245  
 Cys Arg Gly Cys Arg Lys Thr Thr Ala Gly Gly Ala Trp Gln Leu Gln  
 60 65 70

70

ACC ACC GCC GCT CTC ACC GTC AAG TCC ACC ACT CGA CGA CTC CGA GAG 293  
 Thr Thr Ala Ala Leu Thr Val Lys Ser Thr Thr Arg Arg Leu Arg Glu  
           75                          80                          85

5 CTC AAG GAG GTT TAAATTGAAT TCITGCACAAA GACAAACTG TTGCGGGCGG 345  
 Leu Lys Glu Val  
           90

GAGAGAGTGG ATTCAATTCCTT TTTTITTTGTA GATCTGAAGG GATGCCATGT CAACCCCTTTC 405  
 10 GTTCCCCCAA AAAAAAAAAA AAAAAAAAAA AA 437

## (2) INFORMATION FOR SEQ ID NO:47:

15 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 92 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

25 Met Ser Lys Arg Thr Lys Lys Val Gly Ile Thr Gly Lys Tyr Gly Val  
       1                          5                          10                          15

Arg Tyr Gly Ala Ser Leu Arg Lys Thr Val Lys Lys Xaa Glu Val Trp  
           20                          25                          30

30 Gln His Gly Thr Tyr Thr Cys Asp Phe Cys Gly Lys Asp Ala Val Lys  
           35                          40                          45

Arg Thr Ala Val Gly Ile Trp Lys Cys Arg Gly Cys Arg Lys Thr Thr  
       50                          55                          60

Ala Gly Gly Ala Trp Gln Leu Gln Thr Thr Ala Ala Leu Thr Val Lys  
       65                          70                          75                          80

40 Ser Thr Thr Arg Arg Leu Arg Glu Leu Lys Glu Val  
           85                          90

## (2) INFORMATION FOR SEQ ID NO:48:

45 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 509 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
       (A) ORGANISM: Phaffia rhodozyma

60 (ix) FEATURE:  
       (A) NAME/KEY: CDS  
       (B) LOCATION: 35..400  
       (D) OTHER INFORMATION: /product= "PrdINAB7"

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGAGACCTC ACAGCAAGAC TAAGACTCTC AAAC ATG GCT ACC AAG ACC GGC 52  
 70 Met Ala Thr Lys Thr Gly

	1		5	
AAG ACT CGA TCC GCT CTC CAG GAC GTC GTT ACT CGG GAG TAC ACC ATC Lys Thr Arg Ser Ala Leu Gln Asp Val Val Thr Arg Glu Tyr Thr Ile				100
	10		15	20
CAC CTC CAC AAG TAC GTT CAC GGA AGG TCT TTC AAG AAG CGA GCT CCT His Leu His Lys Tyr Val His Gly Arg Ser Phe Lys Lys Arg Ala Pro				148
	25		30	35
TGG GCT GTC AAG TCC ATC CAG GAG TTT GCT CTC AAG TCG ATG GGA ACC Trp Ala Val Lys Ser Ile Gln Glu Phe Ala Leu Lys Ser Met Gly Thr				196
	40		45	50
CGA GAT GTC CGA ATT GAC CCC AAG TTG AAC CAG GCC GTC TGG GGA CAG Arg Asp Val Arg Ile Asp Pro Lys Leu Asn Gln Ala Val Trp Gly Gln				244
	55		60	65
GGT GTC AAG AAC CCC CCC AAG CGA CTC CGA ATC CGA CTT GAG CGA AAG Gly Val Lys Asn Pro Pro Lys Arg Leu Arg Ile Arg Leu Glu Arg Lys				292
	75		80	85
CGA AAC GAC GAG GAG GAT GCT AAG GAC AAG CTC TAC ACT CTT GCT ACC Arg Asn Asp Glu Glu Asp Ala Lys Asp Lys Leu Tyr Thr Leu Ala Thr				340
	90		95	100
GTC GTC CCC GGA GTC ACC AAC TTC AAG GGT CTC CAA ACC GTT GTC GTT Val Val Pro Gly Val Thr Asn Phe Lys Gly Leu Gln Thr Val Val Val				388
	105		110	115
GAC ACC GAG TAATTTTGTC TTGGATTTC ATGACGGTCG ATTCAGCTGT Asp Thr Glu				437
	120			
TTCTTGGGCG CATTCCTCTT ATGCACCTCTG ATGCCCTTCA CGACCNITTT TINTTTCINA				497
TAAATAAAAA AA				509

(2) INFORMATION FOR SEO ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

55	Met	Ala	Thr	Lys	Thr	Gly	Lys	Thr	Arg	Ser	Ala	Leu	Gln	Asp	Val	Val
	1				5					10					15	
	Thr	Arg	Glu	Tyr	Thr	Ile	His	Leu	His	Lys	Tyr	Val	His	Gly	Arg	Ser
				20					25					30		
60	Phe	Lys	Lys	Arg	Ala	Pro	Trp	Ala	Val	Lys	Ser	Ile	Gln	Glu	Phe	Ala
			35					40					45			
	Leu	Lys	Ser	Met	Gly	Thr	Arg	Asp	Val	Arg	Ile	Asp	Pro	Lys	Leu	Asn
		50					55					60				
65	Gln	Ala	Val	Trp	Gly	Gln	Gly	Val	Lys	Asn	Pro	Pro	Lys	Arg	Leu	Arg
	65				70						75					80
	Ile	Arg	Leu	Glu	Arg	Lys	Arg	Asn	Asp	Glu	Glu	Asp	Ala	Lys	Asp	Lys
					85					90					95	

Leu Tyr Thr Leu Ala Thr Val Val Pro Gly Val Thr Asn Phe Lys Gly  
 100 105 110

Leu Gln Thr Val Val Val Asp Thr Glu  
 115 120

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 542 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phaffia rhodozyma*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 18..443

(D) OTHER INFORMATION: /product= "PRcDNA95"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTCGCTATA CATCAAG ATG TCC GTC GCT GTC CAG ACT TTC GGT AAG AAG	50
Met Ser Val Ala Val Gln Thr Phe Gly Lys Lys	
1 5 10	
AAG ACT GCC ACC GCT GTG GCC CAC GCC ACC CCT GGC CGA GGT CTC ATC	98
Lys Thr Ala Thr Ala Val Ala His Ala Thr Pro Gly Arg Gly Leu Ile	
15 20 25	
CGA CTT AAC GGA CAG CCT ATC TCA CTT GCC GAG CCT GCT CTC CTC CGA	146
Arg Leu Asn Gly Gln Pro Ile Ser Leu Ala Glu Pro Ala Leu Leu Arg	
30 35 40	
TAC AAG TAC TAC GAG CCT ATC CTC GTC ATC GGA GCT GAG AAG ATC AAC	194
Tyr Lys Tyr Tyr Glu Pro Ile Leu Val Ile Gly Ala Glu Lys Ile Asn	
45 50 55	
CAG ATC GAC ATC CGA CTC AAG GTC AAG GGT GGA GGA CAC GTC TCC CAG	242
Gln Ile Asp Ile Arg Leu Lys Val Lys Gly Gly Gly His Val Ser Gln	
60 65 70 75	
GTG TAC GCC GTC CGA CAG GCC ATC GGT AAG GCC ATC GTC GCT TAC TAC	290
Val Tyr Ala Val Arg Gln Ala Ile Gly Lys Ala Ile Val Ala Tyr Tyr	
80 85 90	
GCT AAG AAC GTC GAT GCC GCC TCT GCC CTC GAG ATC AAG AAG GCT CTC	338
Ala Lys Asn Val Asp Ala Ala Ser Ala Leu Glu Ile Lys Lys Ala Leu	
95 100 105	
GTC GCC TAC GAC CGA ACC CTC CTC ATC GCC GAT CCC CGA CGA ATG GAG	386
Val Ala Tyr Asp Arg Thr Leu Leu Ile Ala Asp Pro Arg Met Glu	
110 115 120	
CCC AAG AAG TTC CGA GGA CCC GGA GCC CGA GCC CGA GTC CAG AAG TCT	434
Pro Lys Lys Phe Gly Gly Pro Gly Ala Arg Ala Arg Val Gln Lys Ser	
125 130 135	
TAC CGA TAAAGAGTGT TTGTCTGTGT GTCTGGGGG TCATCTATCC AACATCTTTG	490
Tyr Arg	

140

GAAAAANANIT GTTGGGTCA TATGTCATGC CTCCTTATGG AAAAAAAAAA AA

542

5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ser Val Ala Val Gln Thr Phe Gly Lys Lys Lys Thr Ala Thr Ala  
 1 5 10 15

Val Ala His Ala Thr Pro Gly Arg Gly Leu Ile Arg Leu Asn Gly Gln  
 20 25 30

Pro Ile Ser Leu Ala Glu Pro Ala Leu Leu Arg Tyr Lys Tyr Tyr Glu  
 35 40 45

Pro Ile Leu Val Ile Gly Ala Glu Lys Ile Asn Gln Ile Asp Ile Arg  
 50 55 60

Leu Lys Val Lys Gly Gly Gly His Val Ser Gln Val Tyr Ala Val Arg  
 65 70 75 80

Gln Ala Ile Gly Lys Ala Ile Val Ala Tyr Tyr Ala Lys Asn Val Asp  
 85 90 95

Ala Ala Ser Ala Leu Glu Ile Lys Lys Ala Leu Val Ala Tyr Asp Arg  
 100 105 110

Thr Leu Leu Ile Ala Asp Pro Arg Arg Met Glu Pro Lys Lys Phe Gly  
 115 120 125

Gly Pro Gly Ala Arg Ala Arg Val Gln Lys Ser Tyr Arg  
 130 135 140

45

Claims

1. Recombinant DNA comprising a transcription promoter and a downstream sequence to be expressed, in operable linkage therewith,  
5 wherein the transcription promoter comprises a region found upstream of the open reading frame of a highly expressed *Phaffia* gene.
2. Recombinant DNA according to claim 1, wherein said highly expressed *Phaffia* gene is a glycolytic pathway gene.  
10
3. Recombinant DNA according to claim 2, wherein said glycolytic pathway gene is a gene coding for Glyceraldehyde-3-Phosphate Dehydrogenase.
4. Recombinant DNA according to claim 1, wherein said highly expressed *Phaffia* gene is a  
15 ribosomal protein encoding gene.
5. Recombinant DNA comprising a transcription promoter and a downstream sequence to be expressed, in operable linkage therewith,  
wherein the transcription promoter comprises a region found upstream of the open reading  
20 frame encoding a protein as represented by one of the amino acid sequences depicted in any one of SEQIDNOs: 24 to 50.
6. A recombinant DNA according to any one of the preceding claims, wherein said downstream sequence to be expressed is heterologous with respect to the transcription promoter sequence.  
25
7. A recombinant DNA according to any one of claims 1 to 6, wherein the downstream sequence comprises an open reading frame coding for a polypeptide responsible for reduced sensitivity against a selective agent.
- 30 8. A recombinant DNA according to claim 7, wherein said selective agent is G418.
9. A recombinant DNA according to any one of claims 1 to 6, wherein the said downstream sequence to be expressed codes for an enzyme involved in the carotenoid biosynthesis pathway.
- 35 10. A recombinant DNA according to claim 9, wherein said downstream sequence to be expressed encodes an enzyme having an activity selected from the group consisting of isopentenyl pyrophosphate isomerase, geranylgeranyl pyrophosphate synthase, phytoene synthase, phytoene desaturase, and lycopene cyclase.

11. A recombinant DNA according to claim 10, wherein said downstream sequence to be expressed encodes an enzyme having an amino acid sequence selected from the one represented by SEQIDNO: 13, SEQIDNO: 15, SEQIDNO: 17, SEQIDNO: 19, SEQIDNO: 21 or SEQIDNO: 23.
12. A recombinant DNA according to any one of the preceding claims, wherein said recombinant DNA comprises further a transcription terminator downstream from the said DNA sequence to be expressed, in operable linkage therewith.
13. A recombinant DNA according to claim 12, wherein the terminator is a GAPDH-encoding gene terminator fragment.
14. A recombinant DNA according to any one of the preceding claims, wherein the recombinant DNA is in the form of a vector capable of replication and/or integration in a host organism.
15. A recombinant DNA according to claim 14, further comprising *Phaffia* ribosomal RNA encoding DNA.
16. A recombinant DNA according to claim 15, which is linearised by cleaving inside the *Phaffia* ribosomal RNA encoding DNA portion.
17. A microorganism harbouring a recombinant DNA according to any one of the preceding claims.
18. A microorganism according to claim 17, which is *Phaffia rhodozyma*.
19. A microorganism according to claim 18, having the recombinant DNA integrated into its genome in an amount of 50 copies or more.
20. An isolated DNA fragment comprising a *Phaffia* GAPDH-gene, or a functional fragment thereof.
21. Use of a functional fragment according to claim 20 for making a recombinant DNA construct.
22. The use according to claim 21, wherein said fragment is a regulatory region normally located upstream or downstream of the open reading frame coding for GAPDH in *Phaffia rhodozyma*.
23. A method for obtaining a transformed *Phaffia* strain, comprising the steps of  
(a) contacting cells or protoplasts of a *Phaffia* strain with recombinant DNA under conditions conducive to uptake thereof,

said recombinant DNA comprising a transcription promoter and a downstream sequence to be expressed in operable linkage therewith,

(b) identifying *Phaffia rhodozyma* cells or protoplasts having obtained the said recombinant DNA in expressible form,

5 wherein the recombinant DNA is one according to any one of the preceding claims.

24. A method according to claim 23, comprising the additional step of providing an electropulse after contacting of *Phaffia* cells or protoplasts with the said recombinant DNA.

10 25. A transformed *Phaffia* strain obtainable by a method according to any one of the preceding claims, said strain, upon cultivation, being capable of expression of the said downstream sequence, as a consequence of transformation with the said recombinant DNA.

26. A transformed *Phaffia* strain according to claim 25, wherein the said downstream sequence  
15 codes for a pharmaceutical protein.

27. A transformed *Phaffia* strain according to any one of claims 24 to 26, wherein the said *Phaffia* strain contains at least 10, preferably at least 50, copies of the said recombinant DNA integrated into its genome.

20 28. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia rhodozyma*.

29. An isolated DNA sequence according to claim 28, wherein said enzyme has an activity selected  
25 from isopentenyl pyrophosphate isomerase activity, geranylgeranyl pyrophosphate synthase activity, phytoene synthase activity, phytoene desaturase activity and lycopene cyclase activity.

30. An isolated DNA sequence coding for an enzyme having an amino acid sequence selected from the one represented by SEQIDNO: 13, SEQIDNO: 15, SEQIDNO: 17, SEQIDNO: 19, SEQIDNO: 21 or  
30 SEQIDNO: 23.

31. An isolated DNA sequence coding for a variant of an enzyme according to claim 30, said variant being selected from (i) an allelic variant, (ii) an enzyme having one or more amino acid additions, deletions and/or substitutions and still having the stated enzymatic activity.

35

32. An isolated DNA sequence encoding an enzyme involved in the carotenoid biosynthesis pathway selected from:

(i) a DNA sequence as represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16 SEQIDNO: 18; SEQIDNO: 20, or SEQIDNO: 22,



- (ii) an isocoding variant of the DNA sequence represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16, SEQIDNO: 18, SEQIDNO: 20 or SEQIDNO: 22;
- (iii) an allelic variant of a DNA sequence as represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16, SEQIDNO: 18; SEQIDNO: 20 or SEQIDNO: 22;
- 5 (iv) a DNA sequence capable, when bound to nitrocellulose filter and after incubation under hybridising conditions and subsequent washing, of specifically hybridising to a radio-labelled DNA fragment having the sequence represented in SEQIDNO: 12, SEQIDNO: 14, SEQIDNO: 16, SEQIDNO: 18, SEQIDNO: 20 or SEQIDNO: 22, as detectable by autoradiography of the filter after incubation and washing, wherein said incubation under hybridising conditions and subsequent washing is performed by incubating
- 10 the filter-bound DNA at a temperature of at least 50°C, preferably at least 55°C, in the presence of a solution of the said radio-labeled DNA in 0.3 M NaCl, 40 mM Tris-HCl, 2 mM EDTA, 0.1% SDS, pH 7.8 for at least one hour, whereafter the filter is washed at least twice for about 20 minutes in 0.3 M NaCl, 40 mM Tris-HCl, 2 mM EDTA, 0.1% SDS, pH 7.8, at a temperature of 50°C, preferably at least 55°C, prior to autoradiography.
- 15
33. Recombinant DNA comprising an isolated DNA sequence according to any one of claims 27 to 32.
34. Recombinant DNA according to claim 33, wherein said isolated DNA sequence is operably
- 20 linked to a transcription promoter capable of being expressed in a suitable host, said isolated DNA sequence optionally being linked also to a transcription terminator functional in the said host.
35. Recombinant DNA according to claim 34, wherein said host is a *Phaffia* strain.
- 25 36. Recombinant DNA according to any one of claims 33 to 35, wherein the transcription promoter is from a glycolytic pathway gene present in *Phaffia*.
37. Recombinant DNA according to claim 36, wherein said glycolytic pathway gene is a gene coding for Glyceraldehyde-3-Phosphate Dehydrogenase.
- 30
38. Recombinant DNA according to any one of claims 33 to 35, wherein the transcription promoter is from a ribosomal protein encoding gene.
39. Recombinant DNA according to any one of claims 33 to 35, wherein the transcription promoter
- 35 comprises a region found upstream of the open reading frame encoding a protein as represented by one of the amino acid sequences depicted in any one of SEQIDNOs: 24 to 50.

40. Recombinant DNA according to any one of claims 27 to 39, wherein said recombinant DNA comprises further a transcription terminator downstream from the said heterologous DNA sequence to be expressed, in operable linkage therewith, which terminator is a *Phaffia* transcription terminator.
- 5 41. Recombinant DNA according to any one of claims 27 to 40, being in the form of a vector.
42. Use of a vector according to claim 41 to transform a host.
43. Use according to claim 19, wherein the host is a *Phaffia* strain.
- 10 44. A host obtainable by transformation, optionally of an ancestor, using a recombinant DNA according to any one of claims 27 to 41.
45. A host according to claim 44, which is a *Phaffia* strain, preferably a *Phaffia rhodozyma* strain.
- 15 46. A transformed *Phaffia rhodozyma* strain which is capable of overexpressing a DNA sequence encoding an enzyme involved in the carotenoid biosynthesis pathway.
47. A transformed *Phaffia rhodozyma* strain according to claim 46, which produces increased  
20 amounts of astaxanthin relative to its untransformed ancestor.
48. A method for producing an enzyme involved in the carotenoid biosynthesis pathway, by culturing a host according to claim 44 or 45, under conditions conducive to the production of said enzyme.
- 25 49. A method for producing a carotenoid, characterised in that a host according to any one of claims 44 to 47 is cultivated under conditions conducive to the production of the carotenoid.
50. A method according to claim 49, wherein the carotenoid is astaxanthin.
- 30 51. A method for producing a pharmaceutical protein by culturing a transformed *Phaffia* strain according to claim 26 under conditions conducive to the production of the said protein.
52. A method for the isolation of a promoter from a highly expressed gene in *Phaffia*, comprising  
35 the steps of:
- (a) making a cDNA library on mRNA isolated from a *Phaffia* strain grown under desired conditions;
  - (b) determining (part of) the nucleotide sequence of the (partial) cDNAs obtained in step (a);
  - (c) comparing the obtained sequence data in step (b) to known sequence data;

- (d) cloning amplifying putative promoter fragments of the gene located either directly upstream of the open reading frame or directly upstream of the transcription start site of the gene corresponding to the expressed cDNA, and
- (e) verifying whether the promoter sequences obtained give high-level expression in a *Phaffia* strain, by  
5 expressing a suitable marker under the control of the promoter in a transformed *Phaffia* strain.

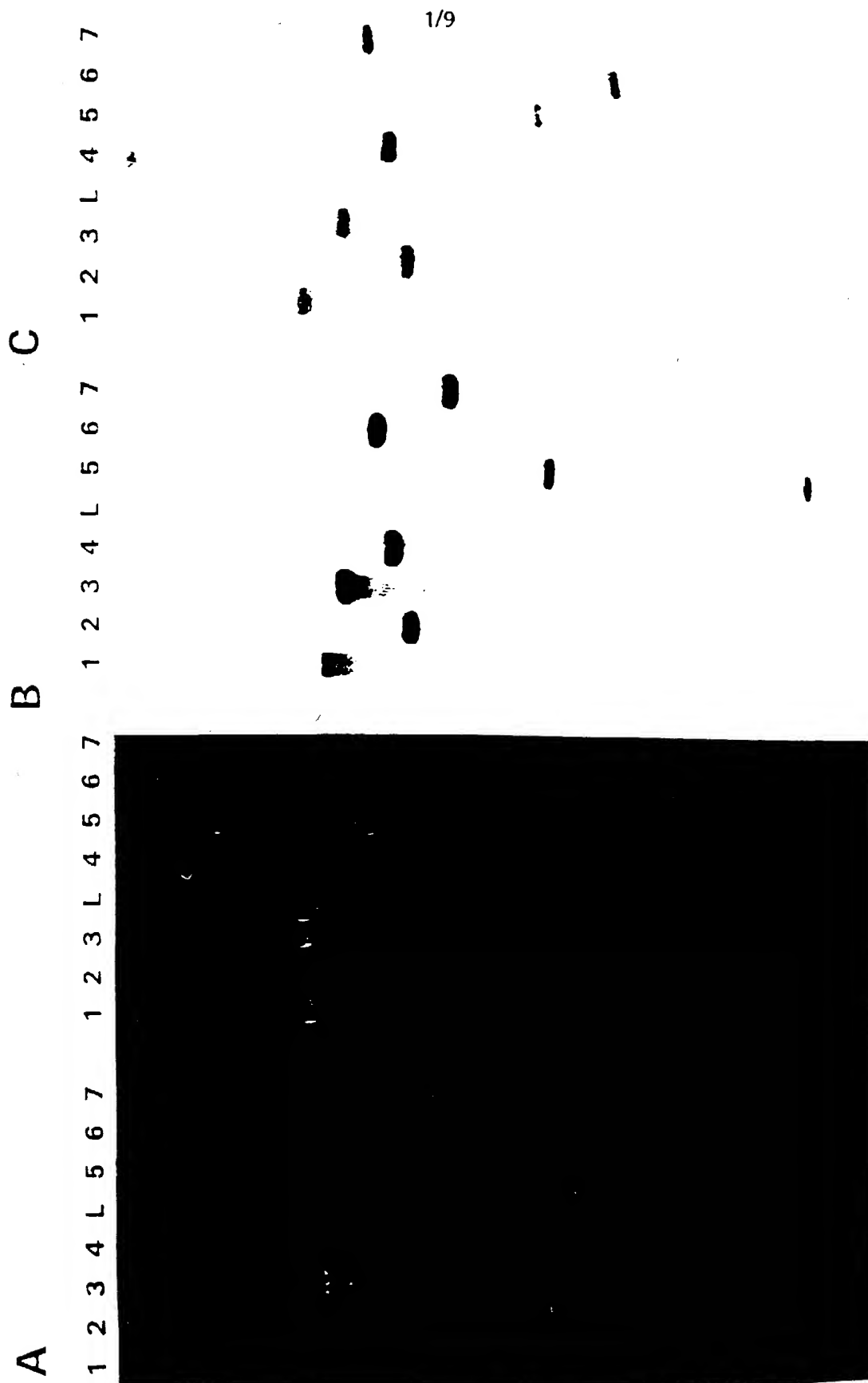
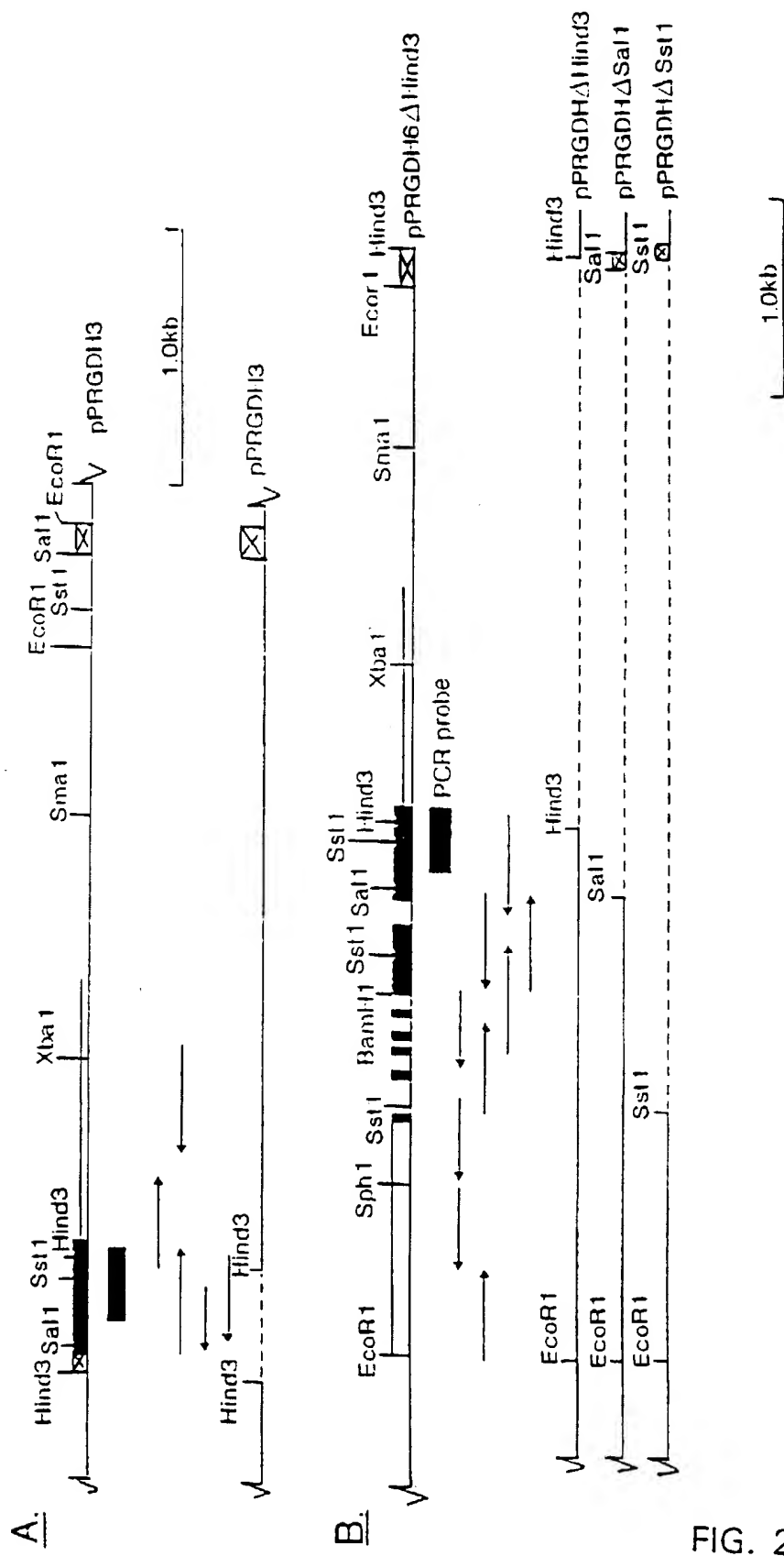


FIG. 1



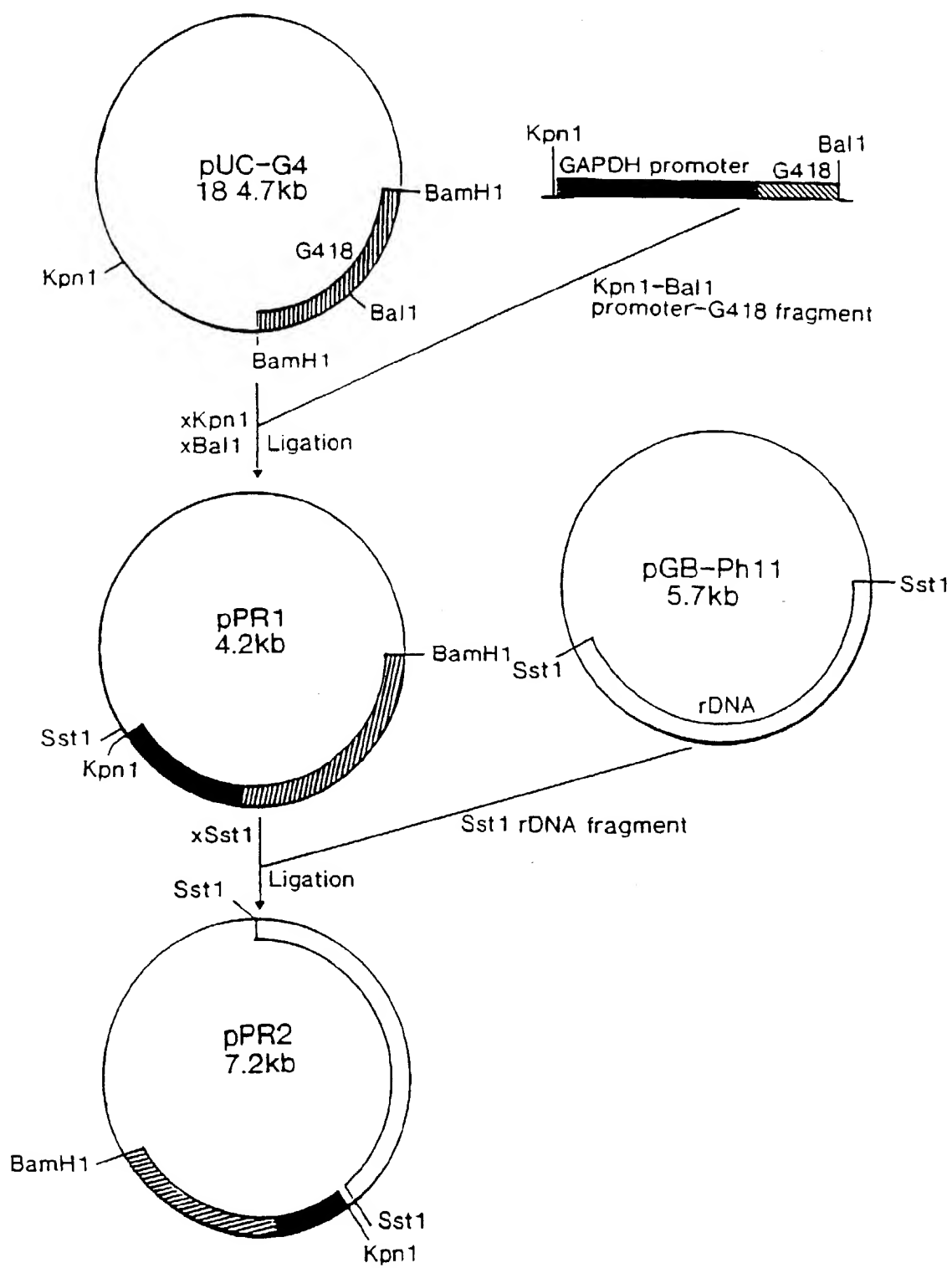


FIG. 3

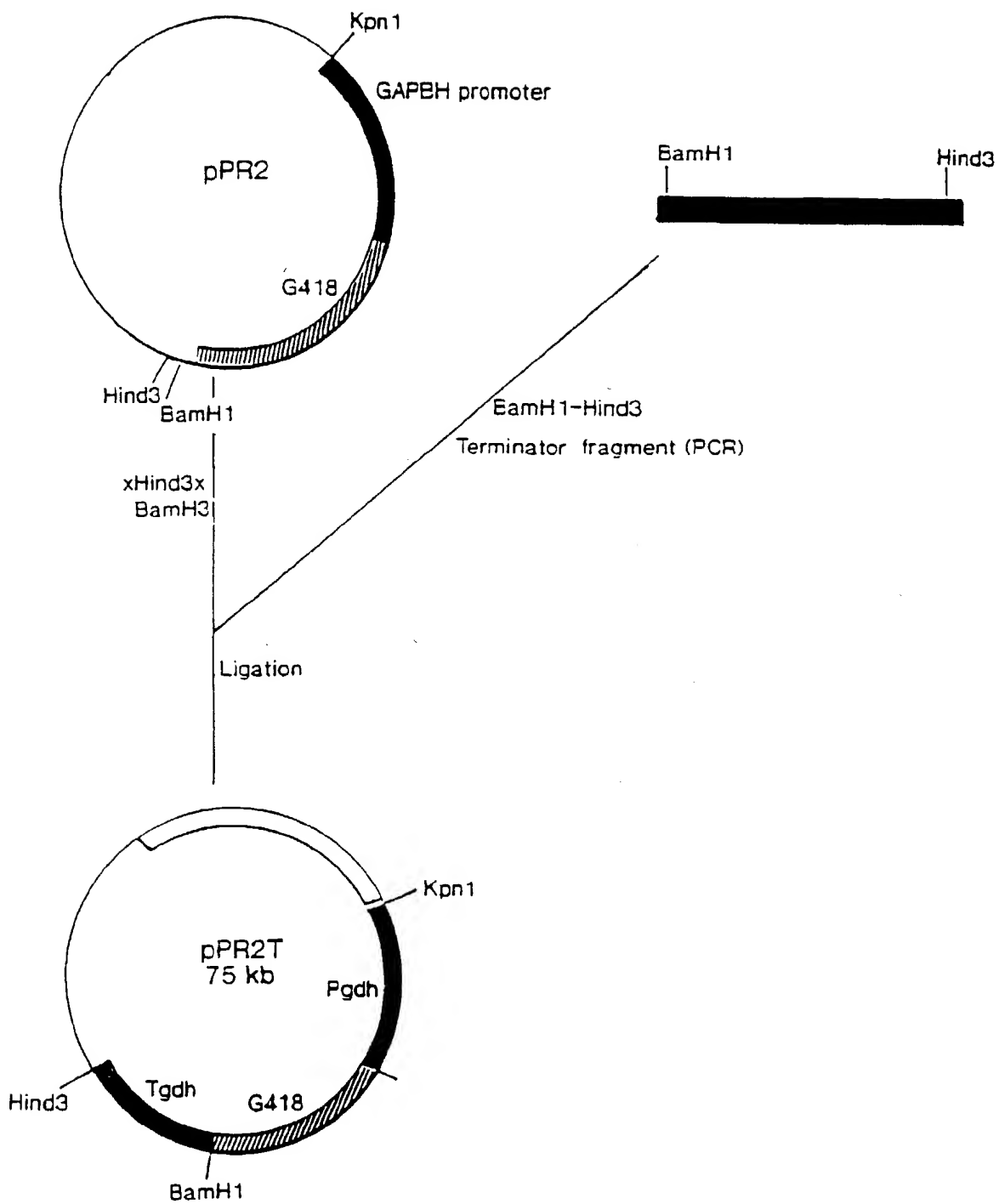


FIG. 4

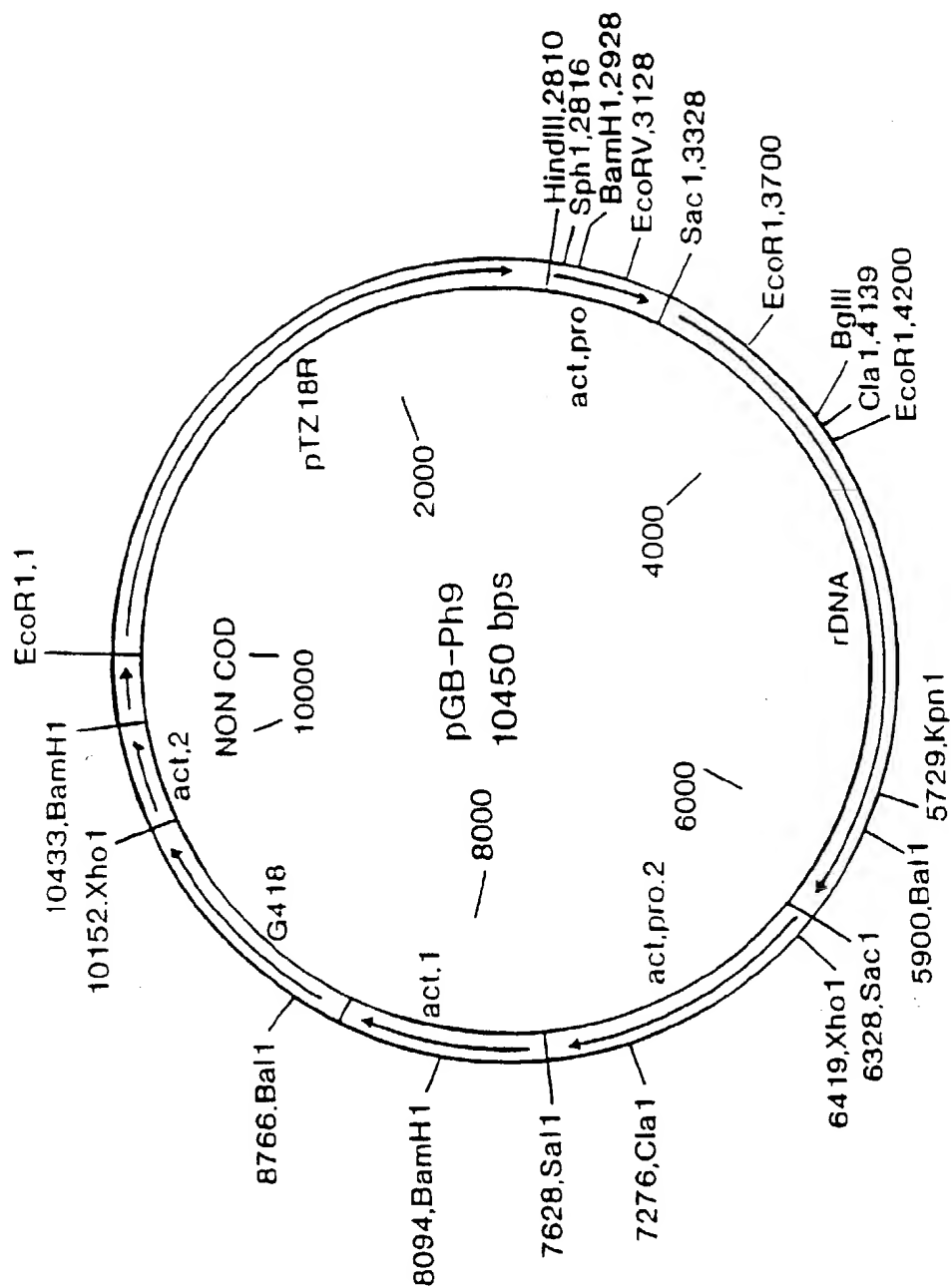


FIG. 5



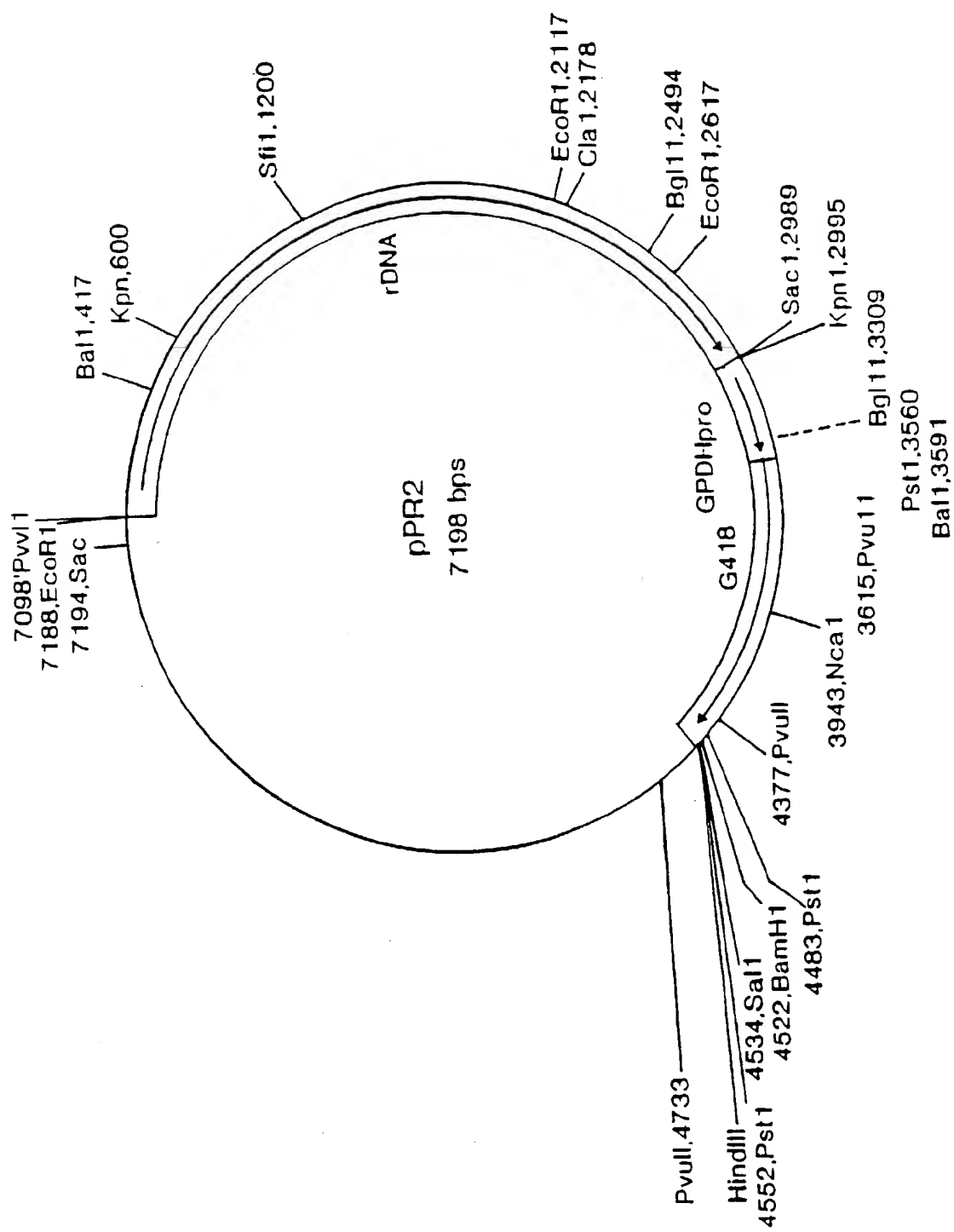


FIG. 6

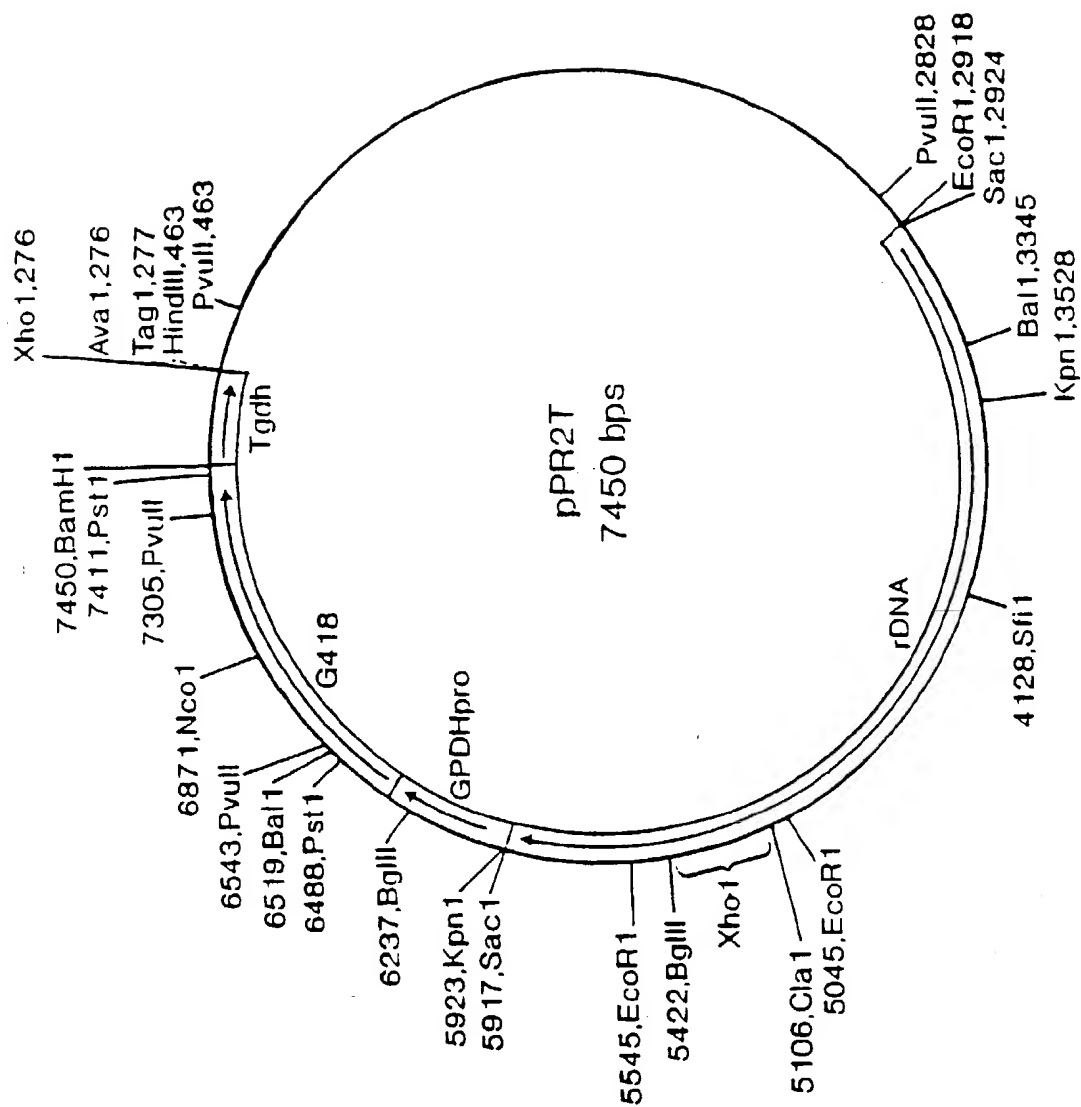


FIG. 7

Carotenoid Biosynthetic Pathway of *Erwinia uredovora*

Farnesyl Pyrophosphate (FPP) + Isopentenyl Pyrophosphate (GPP)

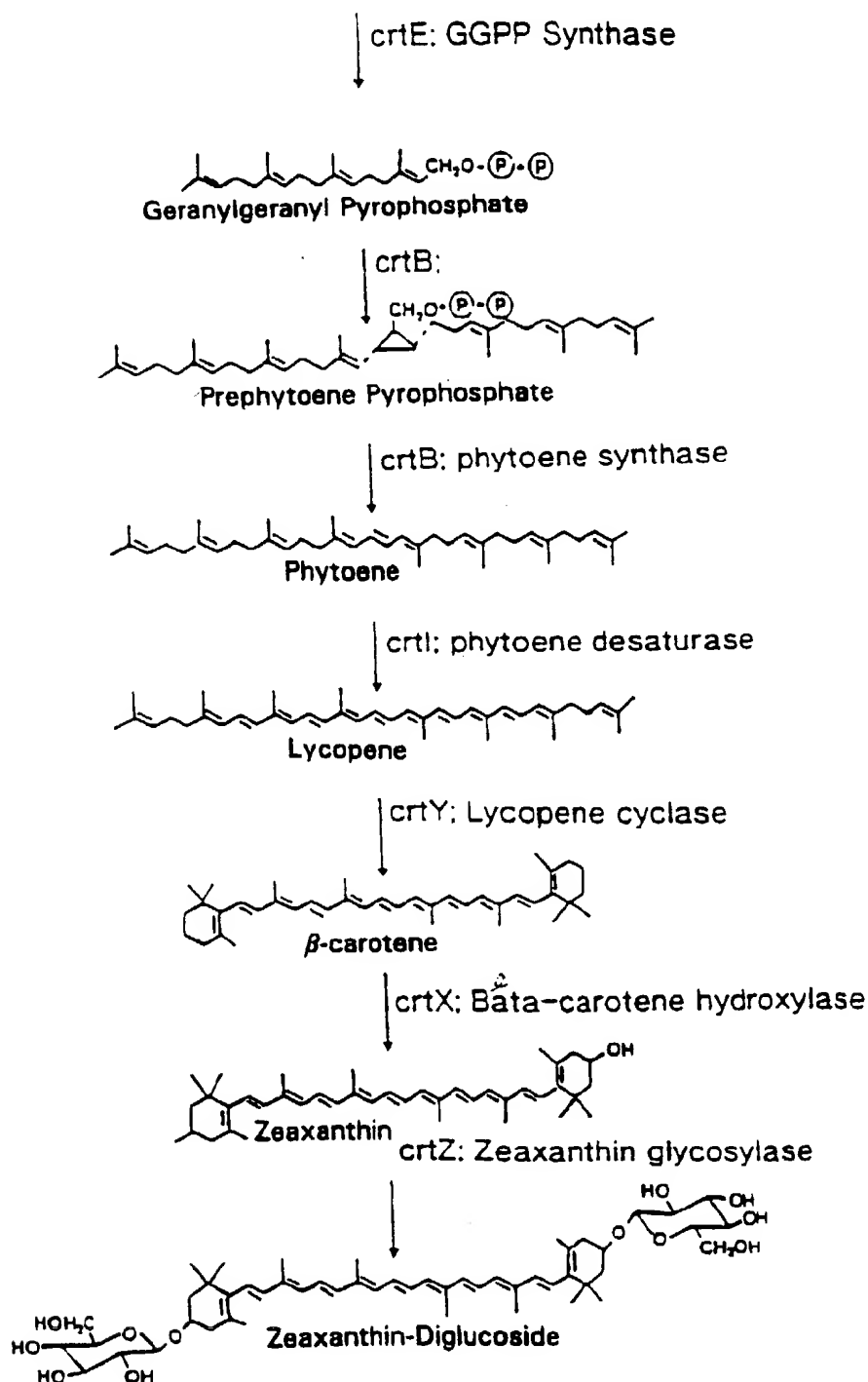
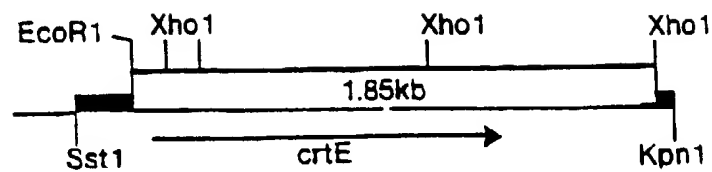
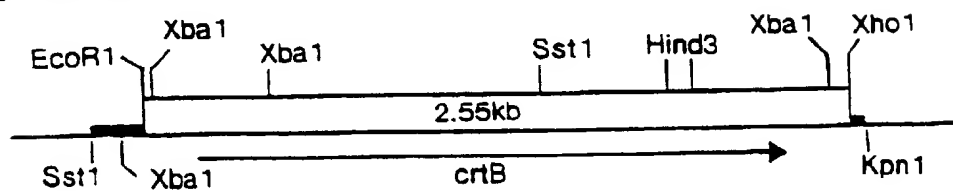


FIG. 8

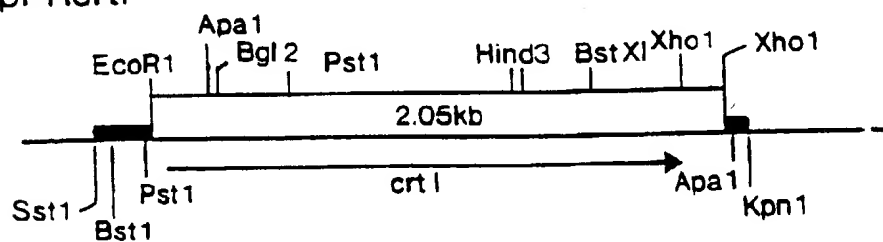
## A pPRcrtE



## B pPRcrtBY



## C pPRcrtI



## pPRcrtY

1.0kb

FIG. 9

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 96/05887

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/81 C12N1/16 C07K14/39 C12N9/02 C12N15/53  
 C12N15/52 C12N15/60 C12P23/00 C12N1/21 //(C12N1/16,  
 C12R1:645), (C12N1/21, C12R1:19)

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ANALES DE LA REAL ACADEMIA DE FARMACIA, vol. 61, no. 4, 1995, pages 463-471, XP000577134 J. ANDRIO ET AL.: "Transformación de Phaffia rhodozyma utilizando el método del acetato de litio."  summary, page 463, page 468, paragraph 3 see page 464, paragraph 1 ---	1,6-8, 12,14, 17-19, 23,25, 27, 33-35, 40,44,45
X	EP 0 590 707 A (GIST BROCADES NV) 6 April 1994 cited in the application	1,6-12, 14, 17-19, 23-25, 27-35, 40-50, 26,51,52
Y	see the whole document ---	
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- \*&\* document member of the same patent family

Date of the actual completion of the international search

5 June 1997

Date of mailing of the international search report

1.2.96.97

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 96/05887

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BIOTECHNOLOGY TECHNIQUES 9 (7). 1995. 509-512. ISSN: 0951-208X, XP000578607 ADRIO J L ET AL: "Transformation of the astaxanthin-producing yeast Phaffia rhodozyma." cited in the application	1,6-12, 14, 17-19, 23,25, 27-35, 40-50
Y	see the whole document	26,51,52
X	--- MOLECULAR & CELLULAR BIOLOGY, vol. 10, no. 10, October 1990, pages 5064-5070, XP000577173 T.J. SCHIDHAUSER ET AL.: "Cloning sequencing and photoregulation of al-1, a carotenoid biosynthetic gene of Neurospora crassa." see the whole document	32-34, 41,42
X	--- THE JOURNAL OF BIOLOGICAL CHEMISTRY., vol. 264, no. 22, 5 August 1989, pages 13109-13113, XP000577175 G.E. BARTLEY ET AL.: "Carotenoid biosynthesis in photosynthetic bacteria" see the whole document	32,33
X	--- MOL. GEN. GENET. , vol. 216, April 1989, pages 254-268, XP000577174 G.A. ARMSTRONG ET AL.: "Nucleotide sequence, organisation and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter capsulatus." see the whole document	32,33
X	--- EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 233, no. 1, 1 October 1995, pages 238-248, XP000578408 BOTELLA J A ET AL: "A CLUSTER OF STRUCTURAL AND REGULATORY GENES FOR LIGHT-INDUCED CAROTENOGENESIS IN MYXOCOCCUS XANTHUS" see the whole document	32,33
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## INTERNATIONAL SEARCH REPORT

Internat'l Application No

PCT/EP 96/05887

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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T	GENE (AMSTERDAM) 184 (1). 1997. 89-97. ISSN: 0378-1119, XP000646757 WERY J ET AL: "High copy number integration into the ribosomal DNA of the yeast Phaffia rhodozyma." see the whole document ---	1-52
A	DATABASE WPI Section Ch, Week 9331 Derwent Publications Ltd., London, GB; Class D16, AN 93-247564 XP002011179 & JP 05 168 465 A (LION CORP) , 2 July 1993 see abstract ---	1-52
A	J. MICROBIOL. BIOTECHNOL. (1992), 2(1), 46-9 CODEN: JOMBES, 1992, XP000571764 KOH, MOO SUK ET AL: "Construction of astaxanthin overproducing strain of Phaffia rhodozyma by protoplast fusion" see the whole document ---	1-52

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# INTERNATIONAL SEARCH REPORT

Internat. Application No.  
PCT/EP 96/05887

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>J. MICROBIOL. BIOTECHNOL. (1995), VOLUME DATE 1995, 5(6), 370-2 CODEN: JOMBES;ISSN: 1017-7825, 1995, XP000571765 CHUN, SOON BAI ET AL: "Cloning of autonomously replicating sequence from Phaffia rhodozyma" see the whole document ---</p>	
A	<p>WO 92 22648 A (VILLADSEN INGRID STAMPE) 23 December 1992 ---</p>	
A	<p>EP 0 474 347 A (QUEST INT) 11 March 1992 ---</p>	
A	<p>FEMS (FED EUR MICROBIOL SOC) MICROBIOL LETT 93 (3). 1992. 221-226. CODEN: FMLED7 ISSN: 0378-1097, XP000569541 CHUN S B ET AL: "STRAIN IMPROVEMENT OF PHAFFIA - RHODOZYMA BY PROTOPLAST FUSION." -----</p>	



# INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP 96/05887

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☒ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International Application No. PCT/EP 96/ 05887

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

1. Recombinant DNA comprising a transcription promoter and downstream region to be expressed where the transcription promoter comprises a region found upstream of a highly expressed *Phaffia* gene, method of transforming a *Phaffia* strain where the transcription promoter is from a **glycolytic pathway gene**, to express a downstream sequence, recombinant DNA thereof, including a selective agent and the transformed *Phaffia* strains : Claims 2, 3, 13, 36 and 37 (completely) and Claims 1, 6 to 14, 17 to 19, 22 to 27, 33 to 35 and 40 to 45 and 51 (partially).
2. Recombinant DNA comprising a transcription promoter and downstream region to be expressed where the transcription promoter comprises a region found upstream of a highly expressed *Phaffia* gene, method of transforming a *Phaffia* strain where the transcription promoter is from a **ribosomal protein**, to express a downstream sequence, recombinant DNA thereof and the transformed *Phaffia* strains: Claims 4, 5, 15, 16, 38 and 39 (completely) and Claims 1, 6 to 12, 14, 17 to 19, 22 to 27, 33 to 35 and 40 to 45 and 51 (partially).
3. An isolated DNA fragment comprising a *Phaffia* GAPDH-gene and use in the construction of a DNA construct: Claims 20 to 21 (completely) and Claim 22 (partially).
4. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia* rhodozyme and recombinant DNA comprising a transcription promoter and the downstream region to be expressed codes for an enzyme involved in the **carotenoid biosynthesis pathway** and the transformed *Phaffia* strains comprising said DNA : Claims 1, 6, 9 to 12, 14, 17 to 19, 23 to 27, 28 to 35 and 40 to 50 (partially)
5. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia* rhodozyme, and recombinant DNA comprising a transcription promoter and the downstream region to be expressed codes for an enzyme involved in the carotenoid biosynthesis pathway and the transformed *Phaffia* strains comprising said DNA, where the enzyme has **isopentenyl pyrophosphate isomerase activity** : Claims 1, 6, 9 to 12, 14, 17 to 19, 23 to 27, 28 to 35 and 40 to 50 (partially)

## INTERNATIONAL SEARCH REPORT

International Application No. PCT/EP 96/ 05887

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

6. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia rhodozyme*, and recombinant DNA comprising a transcription promoter and the downstream region to be expressed codes for an enzyme involved in the carotenoid biosynthesis pathway and the transformed *Phaffia* strains comprising said DNA, where the enzyme has **geranylgeranyl pyrophosphate synthase activity** : Claims 1, 6, 9 to 12, 14, 17 to 19, 23 to 27, 28 to 35 and 40 to 50 {partially}
7. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia rhodozyme* and recombinant DNA comprising a transcription promoter and the downstream region to be expressed codes for an enzyme involved in the carotenoid biosynthesis pathway and the transformed *Phaffia* strains comprising said DNA, where the enzyme has **phytoene synthase activity** : Claims 1, 6, 9 to 12, 14, 17 to 19, 23 to 27, 28 to 35 and 40 to 50 {partially}
8. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia rhodozyme* and recombinant DNA comprising a transcription promoter and the downstream region to be expressed codes for an enzyme involved in the carotenoid biosynthesis pathway and the transformed *Phaffia* strains comprising said DNA, where the enzyme has **phytoene desaturase activity** : Claims 1, 6, 9 to 12, 14, 17 to 19, 23 to 27, 28 to 35 and 40 to 50 {partially}
9. An isolated DNA sequence coding for an enzyme involved in the carotenoid biosynthetic pathway of *Phaffia rhodozyme* and recombinant DNA comprising a transcription promoter and the downstream region to be expressed codes for an enzyme involved in the carotenoid biosynthesis pathway and the transformed *Phaffia* strains comprising said DNA where the enzyme has **lycopene cyclase activity** : Claims 1, 6, 9 to 12, 14, 17 to 19, 23 to 27, 28 to 35 and 40 to 50 {partially}
10. Method for the isolation of a promoter from a gene expressed in *Phaffia* : Claim 52 (completely)

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 96/05887

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